Figure 1

Human
Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

```
        10                    30                     50
AATCTGGCCTCGGAACACGCCATTCTCCGCGCCGCTTCCAATAACCACTAACATCCCTA

        70                    90                    110
ACGAGCATCCGAGCCGAGGGCTCTGCTCGGAAATCGTCCTGGCCCAACTCGGCCCTTCGA

       130                   150                    170
GCTCTCGAAGATTACCGCATCTATTTTTTTTTTCTTTTTTTTCTTTTCCTAGCGCAGATA

       190                   210                    230
AAGTGAGCCCGGAAAGGGAAGGAGGGGGCGGGGACACCATTGCCCTGAAAGAATAAATAA

       250                   270                    290
GTAAATAAACAAACTGGCTCCTCGCCGCAGCTGGACGCGGTCGGTTGAGTCCAGGTTGGG

       310                   330                    350
TCGGACCTGAACCCCTAAAAGCGGAACCGCCTCCCGCCCTCGCCATCCCGGAGCTGAGTC

       370                   390                    410
GCCGGCGGCGGTGGCTGCTGCCAGACCCGGAGTTTCCTCTTTCACTGGATGGAGCTGAAC

       430                   450                    470
TTTGGGCGGCCAGAGCAGCACAGCTGTCCGGGGATCGCTGCACGCTGAGCTCCCTCGGCA

       490                   510                    530
AGACCCAGCGGCGGCTCGGGATTTTTTTGGGGGGGCGGGGACCAGCCCCGCGCCGGCACC

       550                   570                    590
ATGTTCCTGGCGACCCTGTACTTCGCGCTGCCGCTCTTGGACTTGCTCCTGTCGGCCGAA
 M   F   L   A   T   L   Y   F   A   L   P   L   L   D   L   L   L   S   A   E
```

Figure 1 (continued)

```
              610                    630                    650
GTGAGCGGCGGAGACCGCCTGGATTGCGTGAAAGCCAGTGATCAGTGCCTGAAGGAGCAG
 V   S   G   G   D   R   L   D   C   V   K   A   S   D   Q   C   L   K   E   Q


              670                    690                    710
AGCTGCAGCACCAAGTACCGCACGCTAAGGCAGTGCGTGGCGGGCAAGGAGACCAACTTC
 S   C   S   T   K   Y   R   T   L   R   Q   C   V   A   G   K   E   T   N   F


              730                    750                    770
AGCCTGGCATCCGGCCTGGAGGCCAAGGATGAGTGCCGCAGCGCCATGGAGGCCCTGAAG
 S   L   A   S   G   L   E   A   K   D   E   C   R   S   A   M   E   A   L   K


              790                    810                    830
CAGAAGTCGCTCTACAACTGCCGCTGCAAGCGGGGTATGAAGAAGGAGAAGAACTGCCTG
 Q   K   S   L   Y   N   C   R   C   K   R   G   M   K   K   E   K   N   C   L


              850                    870                    890
CGCATTTACTGGAGCATGTACCAGAGCCTGCAGGGAAATGATCTGCTGGAGGATTCCCCA
 R   I   Y   W   S   M   Y   Q   S   L   Q   G   N   D   L   L   E   D   S   P


              910                    930                    950
TATGAACCAGTTAACAGCAGATTGTCAGATATATTCCGGGTGGTCCCATTCATATCAGAT
 Y   E   P   V   N   S   R   L   S   D   I   F   R   V   V   P   F   I   S   D


              970                    990                    1010
GTTTTTCAGCAAGTGGAGCACATTCCCAAAGGGAACAACTGCCTGGATGCAGCGAAGGCC
 V   F   Q   Q   V   E   H   I   P   K   G   N   N   C   L   D   A   A   K   A


              1030                   1050                   1070
TGCAACCTCGACGACATTTGCAAGAAGTACAGGTCGGCGTACATCACCCCGTGCACCACC
 C   N   L   D   D   I   C   K   K   Y   R   S   A   Y   I   T   P   C   T   T


              1090                   1110                   1130
AGCGTGTCCAACGATGTCTGCAACCGCCGCAAGTGCCACAAGGCCCTCCGGCAGTTCTTT
 S   V   S   N   D   V   C   N   R   R   K   C   H   K   A   L   R   Q   F   F
```

Figure 1 (continued)

```
         1150              1170              1190
GACAAGGTCCCGGCCAAGCACAGCTACGGAATGCTCTTCTGCTCCTGCCGGGACATCGCC
  D   K   V   P   A   K   H   S   Y   G   M   L   F   C   S   C   R   D   I   A


         1210              1230         -    1250
TGCACAGAGCGGAGGCGACAGACCATCGTGCCTGTGTGCTCCTATGAAGAGAGGGAGAAG
  C   T   E   R   R   R   Q   T   I   V   P   V   C   S   Y   E   E   R   E   K


         1270              1290              1310
CCCAACTGTTTGAATTTGCAGGACTCCTGCAAGACGAATTACATCTGCAGATCTCGCCTT
  P   N   C   L   N   L   Q   D   S   C   K   T   N   Y   I   C   R   S   R   L


         1330              1350              1370
GCGGATTTTTTTACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAGCTGTCTAAAGGAA
  A   D   F   F   T   N   C   Q   P   E   S   R   S   V   S   S   C   L   K   E


         1390              1410              1430
AACTACGCTGACTGCCTCCTCGCCTACTCGGGGCTTATTGGCACAGTCATGACCCCCAAC
  N   Y   A   D   C   L   L   A   Y   S   G   L   I   G   T   V   M   T   P   N


         1450              1470         -    1490
TACATAGACTCCAGTAGCCTCAGTGTGGCCCCATGGTGTGACTGCAGCAACAGTGGGAAC
  Y   I   D   S   S   S   L   S   V   A   P   W   C   D   C   S   N   S   G   N


         1510              1530              1550
GACCTAGAAGAGTGCTTGAAATTTTTTGAATTTCTTCAAGGACAATACATGTCTTAAAAAT
  D   L   E   E   C   L   K   F   L   N   F   F   K   D   N   T   C   L   K   N


         1570              1590              1610
GCAATTCAAGCCTTTGGCAATGGCTCCGATGTGACCGTGTGGCAGCCAGCCTTCCCAGTA
  A   I   Q   A   F   G   N   G   S   D   V   T   V   W   Q   P   A   F   P   V


         1630              1650              1670
CAGACCACCACTGCCACTACCACCACTGCCCTCCGGGTTAAGAACAAGCCCCTGGGGCCA
  Q   T   T   T   A   T   T   T   T   A   L   R   V   K   N   K   P   L   G   P
```

Figure 1 (continued)

```
        1690                  1710                  1730
GCAGGGTCTGAGAATGAAATTCCCACTCATGTTTTGCCACCGTGTGCAAATTTACAGGCA
 A   G   S   E   N   E   I   P   T   H   V   L   P   P   C   A   N   L   Q   A


        1750                  1770                  1790
CAGAAGCTGAAATCCAATGTGTCGGGCAATACACACCTCTGTATTTCCAATGGTAATTAT
 Q   K   L   K   S   N   V   S   G   N   T   H   L   C   I   S   N   G   N   Y


        1810                  1830                  1850
GAAAAAGAAGGTCTCGGTGCTTCCAGCCACATAACCACAAAATCAATGGCTGCTCCTCCA
 E   K   E   G   L   G   A   S   S   H   I   T   T   K   S   M   A   A   P   P


        1870                  1890                  1910
AGCTGTGGTCTGAGCCCACTGCTGGTCCTGGTGGTAACCGCTCTGTCCACCCTATTATCT
 S   C   G   L   S   P   L   L   V   L   V   V   T   A   L   S   T   L   L   S


        1930                  1950                  1970
TTAACAGAAACATCATAGCTGCATTAAAAAAATACAATATGGACATGTAAAAAGACAAAA
 L   T   E   T   S   *


        1990                  2010                  2030
ACCAAGTTATCTGTTTCCTGTTCTCTTGTATAGCTGAAATTCCAGTTTAGGAGCTCAGTT


        2050                  2070                  2090
GAGAAACAGTTCCATTCAACTGGAACATTTTTTTTTTT.CCTTTTAAGAAAGCTTCTTGT


        2110                  2130                  2150
GATCCTT.GGGGCTTCTGTGAAAAACCTGATGCAGTGCTCCATCCAAACTCAGAAGGCTT


        2170                  2190                  2210
TGGGATATGCTGTATTTTAAAGGGACAGTTTGTAACTTGGGCTGTAAAGCAAACTGGGGC


        2230                  2250                  2270
TGTGTTTTCGATGATGATGAT.ATCATGAT.ATGAT........................


        2290                  2310                  2330
...............GATTTTAACAGTTTTACTTCTGGCCTTTCCTAGCTAGAGAAGGAG
```

Figure 1 (continued)

```
        2350              2370              2390
TTAATATTTCTAAGGTAACTCCCATATCTCCTTTAATGACATTGATTTCTAATGATATAA


        2410              2430              2450
ATTTCAGCCTACATTGATGCCAAGCTTTTTTGCCACAAAGAAGATTCTTACCAAGAGTGG


        2470              2490              2510
GCTTTGTGGAAACAGCTGGTACTGATGTTCACCTTTATATATGTACTAGCATTTTCCACG


        2530              2550
CTGATGTTTATGTACTGTAAACAGTTCTGCACTCTTGTACAAAAGAAAA
```

Note: The dots in the above sequence listing from 2240 to 2300 indicate positions of divergence between different receptor clones. One of the human clones contains an insert of 39 nucleotides from 2258 to 2297 and has different bases at positions 2244 and 2253.

Figure 2

Human
Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

```
M  F  L  A  T  L  Y  F  A  L  P  L  L  D  L  L  L  S  A  E   20

V  S  G  G  D  R  L  D  C  V  K  A  S  D  Q  C  L  K  E  Q   40

S  C  S  T  K  Y  R  T  L  R  Q  C  V  A  G  K  E  T  N  F   60

S  L  A  S  G  L  E  A  K  D  E  C  R  S  A  M  E  A  L  K   80

Q  K  S  L  Y  N  C  R  C  K  R  G  M  K  K  E  K  N  C  L   100

R  I  Y  W  S  M  Y  Q  S  L  Q  G  N  D  L  L  E  D  S  P   120

Y  E  P  V  N  S  R  L  S  D  I  F  R  V  V  P  F  I  S  D   140

V  F  Q  Q  V  E  H  I  P  K  G  N  N  C  L  D  A  A  K  A   160

C  N  L  D  D  I  C  K  K  Y  R  S  A  Y  I  T  P  C  T  T   180

S  V  S  N  D  V  C  N  R  R  K  C  H  K  A  L  R  Q  F  F   200

D  K  V  P  A  K  H  S  Y  G  M  L  F  C  S  C  R  D  I  A   220

C  T  E  R  R  R  Q  T  I  V  P  V  C  S  Y  E  E  R  E  K   240

P  N  C  L  N  L  Q  D  S  C  K  T  N  Y  I  C  R  S  R  L   260

A  D  F  F  T  N  C  Q  P  E  S  R  S  V  S  S  C  L  K  E   280

N  Y  A  D  C  L  L  A  Y  S  G  L  I  G  T  V  M  T  P  N   300

Y  I  D  S  S  S  L  S  V  A  P  W  C  D  C  S  N  S  G  N   320

D  L  E  E  C  L  K  F  L  N  F  F  K  D  N  T  C  L  K  N   340

A  I  Q  A  F  G  N  G  S  D  V  T  V  W  Q  P  A  F  P  V   360

Q  T  T  T  A  T  T  T  T  A  L  R  V  K  N  K  P  L  G  P   380

A  G  S  E  N  E  I  P  T  H  V  L  P  P  C  A  N  L  Q  A   400

Q  K  L  K  S  N  V  S  G  N  T  H  L  C  I  S  N  G  N  Y   420

E  K  E  G  L  G  A  S  S  H  I  T  T  K  S  M  A  A  P  P   440

S  C  G  L  S  P  L  L  V  L  V  V  T  A  L  S  T  L  L  S   460

L  T  E  T  S  *  465
```

Figure 3

Rat
Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

```
          10                      30               · ·      50
AGCTCGCTCTCCCGGGGCAGTGGTGTGGATGCACCGGAGTTCGGGCGCTGGGCAAGTTGG


          70                      90            _         110
GTCGGAACTGAACCCCTGAAAGCGGGTCCGCCTCCCGCCCTCGCGCCCGCCCGGATCTGA


          130                     150                     170
GTCGCTGGCGGCGGTGGGCGGCAGAGCGACGGGGAGTCTGCTCTCACCCTGGATGGAGCT


          190                     210                     230
GAACTTTGAGTGGCCAGAGGAGCGCAGTCGCCCGGGGATCGCTGCACGCTGAGCTCTCTC


          250                     270                     290
CCCGAGACCGGGCGGCGGCTTTGGATTTTGGGGGGGCGGGGACCAGCTGCGCGGCGGCAC


          310                     330                     350
CATGTTCCTAGCCACTCTGTACTTCGCGCTGCCACTCCTGGATTTGCTGATGTCCGCCGA
 M   F   L   A   T   L   Y   F   A   L   P   L   L   D   L   L   M   S   A   E


          370                     390                     410
GGTGAGTGGTGGAGACCGTCTGGACTGTGTGAAAGCCAGCGATCAGTGCCTGAAGGAACA
 V   S   G   G   D   R   L   D   C   V   K   A   S   D   Q   C   L   K   E   Q


          430                     450                     470
GAGCTGCAGCACCAAGTACCGCACACTAAGGCAGTGCGTGGCGGGCAAGGAAACCAACTT
 S   C   S   T   K   Y   R   T   L   R   Q   C   V   A   G   K   E   T   N   F


          490                     510                     530
CAGCCTGACATCCGGCCTTGAGGCCAAGGATGAGTGCCGTAGCGCCATGGAGGCCTTGAA
 S   L   T   S   G   L   E   A   K   D   E   C   R   S   A   M   E   A   L   K
```

Figure 3 (continued)

```
            550               570                   590
GCAGAAGTCTCTGTACAACTGCCGCTGCAAGCGGGGCATGAAGAAAGAGAAGAATTGTCT
 Q   K   S   L   Y   N   C   R   C   K   R   G   M   K   K   E   K   N   C   L
```

```
            610               630                   650
GCGTATCTACTGGAGCATGTACCAGAGCCTGCAGGGAAATGACCTCCTGGAAGATTCCCC
 R   I   Y   W   S   M   Y   Q   S   L   Q   G   N   D   L   L   E   D   S   P
```

```
            670               690                   710
GTATGAGCCGGTTAACAGCAGGTTGTCAGATATATTCCGGGCAGTCCCGTTCATATCAGA
 Y   E   P   V   N   S   R   L   S   D   I   F   R   A   V   P   F   I   S   D
```

```
            730               750                   770
TGTTTTCCAGCAAGTGGAACACATTTCCAAAGGGAACAACTGCCTGGACGCAGCCAAGGC
 V   F   Q   Q   V   E   H   I   S   K   G   N   N   C   L   D   A   A   K   A
```

```
            790               810                   830
CTGCAACCTGGACGACACCTGTAAGAAGTACAGGTCGGCCTACATCACCCCCTGCACCAC
 C   N   L   D   D   T   C   K   K   Y   R   S   A   Y   I   T   P   C   T   T
```

```
            850               870                   890
CAGCATGTCCAACGAGGTCTGCAACCGCCGTAAGTGCCACAAGGCCCTCAGGCAGTTCTT
 S   M   S   N   E   V   C   N   R   R   K   C   H   K   A   L   R   Q   F   F
```

```
            910               930                   950
CGACAAGGTTCCGGCCAAGCACAGCTACGGGATGCTCTTCTGCTCCTGCCGGGACATCGC
 D   K   V   P   A   K   H   S   Y   G   M   L   F   C   S   C   R   D   I   A
```

```
            970               990                   1010
CTGCACCGAGCGGCGGCGACAGACTATCGTCCCCGTGTGCTCCTATGAAGAACGAGACAG
 C   T   E   R   R   R   Q   T   I   V   P   V   C   S   Y   E   E   R   E   R
```

```
            1030              1050                  1070
GCCCAACTGCCTGAGTCTGCAAGACTCCTGCAAGACCAATTACATCTGCAGATCTCGCCT
 P   N   C   L   S   L   Q   D   S   C   K   T   N   Y   I   C   R   S   R   L
```

Figure 3 (continued)

```
          1090                  1110                  1130
TGCAGATTTTTTTACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAACTGTCTTAAGGA
  A   D   F   F   T   N   C   Q   P   E   S   R   S   V   S   N   C   L   K   E


          1150                  1170          -     1190
GAACTACGCAGACTGCCTCCTGGCCTACTCGGGACTGATTGGCACAGTCATGACTCCCAA
  N   Y   A   D   C   L   L   A   Y   S   G   L   I   G   T   V   M   T   P   N


          1210                  1230                  1250
CTACGTAGACTCCAGCAGCCTCAGCGTGGCACCATGGTGTGACTGCAGCAACAGCGGCAA
  Y   V   D   S   S   S   L   S   V   A   P   W   C   D   C   S   N   S   G   N


          1270                  1290                  1310
TGACCTGGAAGACTGCTTGAAATTTCTGAATTTTTTTAAGGACAATACTTGTCTCAAAAA
  D   L   E   D   C   L   K   F   L   N   F   F   K   D   N   T   C   L   K   N


          1330                  1350                  1370
TGCAATTCAAGCCTTTGGCAATGGCTCAGATGTGACCATGTGGCAGCCAGCCCCTCCAGT
  A   I   Q   A   F   G   N   G   S   D   V   T   M   W   Q   P   A   P   P   V


          1390                  1410          -       1430
CCAGACCACCACTGCCACCACTACCACTGCCTTCCGGGTCAAGAACAAGCCTCTGGGGCC
 ·Q   T   T   T   A   T   T   T   T   A   F   R   V   K   N   K   P   L   G   P


          1450                  1470                  1490
AGCAGGGTCTGAGAATGAGATCCCCACACACGTTTTACCACCCTGTGCGAATTTGCAGGC
  A   G   S   E   N   E   I   P   T   H   V   L   P   P   C   A   N   L   Q   A


          1510                  1530                  1550
TCAGAAGCTGAAATCCAATGTGTCGGGTAGCACACACCTCTGTCTTTCTGATAGTGATTT
  Q   K   L   K   S   N   V   S   G   S   T   H   L   C   L   S   D   S   D   F


          1570              ·· 1590                  1610
CGGAAAGGATGGTCTCGCTGGTGCCTCCAGCCACATAACCACAAAATCAATGGCTGCTCC
  G   K   D   G   L   A   G   A   S   S   H   I   T   T   K   S   M   A   A   P
```

Figure 3 (continued)

```
        1630                1650                1670
TCCCAGCTGCAGTCTGAGCTCACTGCCGGTGCTGATGCTCACCGCCCTTGCTGCCCTGTT
  P   S   C   S   L   S   S   L   P   V   L   M   L   T   A   L   A   A   L   L


        1690                1710                1730
ATCTGTATCGTTGGCAGAAACGTCGTAGCTGCATCCGGGAAAACAGTATGAAAAGACAAA
  S   V   S   L   A   E   T   S   *


        1750                1770                1790
AGAGAACCAAGTATTCTGTCCCTGTCCTCTTGTATATCTGAAAATCCAGTTTTAAAAGCT


        1810                1830                1850
CCGTTGAGAAGCAGTTTCACCCAACTGGAACTCTTTCCTTGTTTTTAAGAAAGCTTGTGG


        1870                1890                1910
CCCTCAGGGGCTTCTGTTGAAGAACTGCTACAGGGCTAATTCCAAACCCATAAGGCTCTG


        1930                1950                1970
GGGCGTGGTGCGGCTTAAGGGGACCATTTGCACCATGTAAAGCAAGCTGGGCTTATCATG


        1990                2010                2030
TGTTTGATGGTGAGGATGGTAGTGGTGATGATGATGGTAATTTTAACAGCTTGAACCCTG


        2050                2070                2090
TTCTCTCTACTGGTTAGGAACAGGAGATACTATTGATAAAGATTCTTCCATGTCTTACTC


        2110                2130
AGCAGCATTGCCTTCTGAAGACAGGCCCGCAGCCGTCG
```

Figure 4

Rat
Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

M F L A T L Y F A L P L L D L L M S A E 20

V S G G D R L D C V K A S D Q C L K E Q 40

S C S T K Y R T L R Q C V A G K E T N F 60

S L T S G L E A K D E C R S A M E A L K 80

Q K S L Y N C R C K R G M K K E K N C L 100

R I Y W S M Y Q S L Q G N D L L E D S P 120

Y E P V N S R L S D I F R A V P F I S D 140

V F Q Q V E H I S K G N N C L D A A K A 160

C N L D D T C K K Y R S A Y I T P C T T 180

S M S N E V C N R R K C H K A L R Q F F 200

D K V P A K H S Y G M L F C S C R D I A 220

C T E R R R Q T I V P V C S Y E E R E R 240

P N C L S L Q D S C K T N Y I C R S R L 260

A D F F T N C Q P E S R S V S N C L K E 280

N Y A D C L L A Y S G L I G T V M T P N 300

Y V D S S S L S V A P W C D C S N S G N 320

D L E D C L K F L N F F K D N T C L K N 340

A I Q A F G N G S D V T M W Q P A P P V 360

Q T T T A T T T T A F R V K N K P L G P 380

A G S E N E I P T H V L P P C A N L Q A 400

Q K L K S N V S G S T H L C L S D S D F 420

G K D G L A G A S S H I T T K S M A A P 440

P S C S L S S L P V L M L T A L A A L L 460

S V S L A E T S *   468

Figure 5

Human GDNF receptor Clones -- Alignment to generate consensus sequence

```
              -237                               .  .                  -188
      Gdnfr   AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA
  Hsgr-21af     TCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA
  Hsgr-21bf   AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA
     21acon     TCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA
     21bcon   AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA


              -187                                                     -138
      Gdnfr   ACATCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG
  Hsgr-21af   ACATCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG
  Hsgr-21bf   ACATCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG
     21acon   ACATCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG
     21bcon   ACATCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG


              -137                               _  .                  -88
      Gdnfr   GCCCAACTCG GCCCTTCGAG CTCTCGAAGA TTACCGCATC TATTTTTTTT
  Hsgr-21af   GCCCAACTCG GCCCTTCGAG CTCTCGAAGA TTACCGCATC TATTTTTTTT
  Hsgr-21bf   GCCCAACTCG GCCCTTCGAG CTCTCGAAGA TTACCGCATC TATTTTTTTT
     21acon   GCCCAACTCG GCCCTTCGAG CTCTCGAAGA TTACCGCATC TATTTTTTTT
     21bcon   GCCCAACTCG GCCCTTCGAG CTCTCGAAGA TTACCGCATC TATTTTTTTT


              -87                                                      -38
      Gdnfr   TTCTTTTTTT TCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
  Hsgr-21af   TTCTTTTTTT TCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
  Hsgr-21bf   TTCTTTTTTT TCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
     21acon   TTCTTTTTTT TCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
     21bcon   TTCTTTTTTT TCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
```

Figure 5 (continued)

```
                 -37                                                    12
      Gdnfr     GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA

  Hsgr-21af     GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA

  Hsgr-21bf     GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA

     21acon     GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA

     21bcon     GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA


                 13                                                     62
      Gdnfr     AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT

  Hsgr-21af     AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT

  Hsgr-21bf     AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT

     21acon     AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT

     21bcon     AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT


                 63                                                    112
      Gdnfr     CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG

  Hsgr-21af     CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG

  Hsgr-21bf     CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG

     21acon     CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG

     21bcon     CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG


                 113                                                   162
      Gdnfr     AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT

  Hsgr-21af     AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT

  Hsgr-21bf     AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT

     21acon     AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT

     21bcon     AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT


                 163                                                   212
      Gdnfr     TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG

  Hsgr-21af     TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG

  Hsgr-21bf     TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG

     21acon     TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG

     21bcon     TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
```

Figure 5 (continued)

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          213                                                    262
   Gdnfr  GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
Hsgr-21af  GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
Hsgr-21bf  GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
   21acon  GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
   21bcon  GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA


          263                                                    312
   Gdnfr  TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACCA TGTTCCTGGC
Hsgr-21af  TTTTTTTGGG
Hsgr-21bf  TTTTTTTGGG
   21acon  TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACCA TGTTCCTGGC
   21bcon  TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACCA TGTTCCTGGC


          313                                                    362
   Gdnfr  GaCCCTGTAC TTCGCGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG
   21acon  GNCCCTGTAC TTCGCGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG
   21bcon  GACCCTGTAC TTCGCGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG


          363                                                    412
   Gdnfr  TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG
   21acon  TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG
   21bcon  TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG


          413                                                    462
   Gdnfr  AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC
   21acon  AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC
   21bcon  AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC


          463                                                    512
   Gdnfr  GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
   21acon  GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
   21bcon  GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
```

Figure 5 (continued)

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        513                                                    562
Gdnfr   AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC
21acon  AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC
21bcon  AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC


        563                                   .                612
Gdnfr   CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTTACTG
21acon  CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTTACTG
21bcon  CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTTACTG


        613                                                    662
Gdnfr   GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT
21acon  GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT
21bcon  GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT


        663                                                    712
Gdnfr   ATGAACCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTC
21acon  ATGAACCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTC
21bcon  ATGAACCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTC


        713                                                    762
Gdnfr   ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACTG
21acon  ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACTG
21bcon  ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACTG


        763                                                    812
Gdnfr   CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTTGC AAGAAGTACA
21acon  CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTTGC AAGAAGTACA
21bcon  CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTTGC AAGAAGTACA


         813                                                   862
Gdnfr    GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA .GATGTCTGC
Hsgr-29a  GTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA TGATGTCTGC
21acon   GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA CGATGTCTGC
21bcon   GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA CGATGTCTGC
29brc     GTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA TGATGTCTGC
```

Figure 5 (continued)

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              863                                                   912
     Gdnfr    AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
  Hsgr-29a    AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
    21acon    AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
    21bcon    AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
     29brc    AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC


              913                                                   962
     Gdnfr    GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
  Hsgr-29a    GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
    21acon    GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
    21bcon    GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
     29brc    GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT


              963                                                  1012
     Gdnfr    GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
  Hsgr-29a    GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
    21acon    GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
    21bcon    GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
     29brc    GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG


              1013                                                 1062
     Gdnfr    AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
  Hsgr-21ar                                   GAATTTGCAG GACTCCTGCA AGACGAATTA
  Hsgr-21br                                                                  A
  Hsgr-29a    AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
    21acon    AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
    21bcon    AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
     29brc    AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
```

Figure 5 (continued)

```
          1063                                                    1112
   Gdnfr   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
Hsgr-21ar  CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
Hsgr-21br  CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
Hsgr-29a   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
  21acon   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
  21bcon   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
   29brc   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT


          1113                                                    1162
   Gdnfr   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
Hsgr-21ar  CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
Hsgr-21br  CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
Hsgr-29a   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
  21acon   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
  21bcon   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
   29brc   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC


          1163                                                    1212
   Gdnfr   GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
Hsgr-21ar  GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
Hsgr-21br  GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
Hsgr-29a   GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
  21acon   GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
  21bcon   GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
   29brc   GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC


          1213                                                    1262
   Gdnfr   CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
  Hsgr-2                                                     TGGGAACG
Hsgr-21ar  CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
Hsgr-21br  CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
Hsgr-29a   CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
  21acon   CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
  21bcon   CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
   29brc   CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
```

Figure 5 (continued)

```
           1263                                                    1312
   Gdnfr   ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
   Hsgr-2  ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
   Hsgr-9           A GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
Hsgr-21ar  ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
Hsgr-21br  ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
 Hsgr-29a  ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
   21acon  ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
   21bcon  ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
    29brc  ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT


           1313                                                    1362
   Gdnfr   CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
   Hsgr-2  CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
   Hsgr-9  CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
Hsgr-21ar  CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
Hsgr-21br  CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
 Hsgr-29a  CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
   21acon  CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
   21bcon  CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
    29brc  CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG


           1363                                                    1412
   Gdnfr   GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCaCTACC ACCACTGCCC
   Hsgr-2  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
   Hsgr-9  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
Hsgr-21ar  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
Hsgr-21br  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
 Hsgr-29a  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCGCTACC ACCACTGCCC
   21acon  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
   21bcon  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
    29brc  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCGCTACC ACCACTGCCC
```

Figure 5 (continued)

```
            1413                                                    1462
    Gdnfr   TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
   Hsgr-2   TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
   Hsgr-9   TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
 Hsgr-21ar  TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
 Hsgr-21br  TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
 Hsgr-29a   TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
   21acon   TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
   21bcon   TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
    29brc   TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT


            1463                                                    1512
    Gdnfr   CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
   Hsgr-2   CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
   Hsgr-9   CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
 Hsgr-21ar  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
 Hsgr-21br  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
 Hsgr-29a   CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
   21acon   CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
   21bcon   CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
    29brc   CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA


            1513                                                    1562
    Gdnfr   ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
   Hsgr-2   ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
   Hsgr-9   ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
 Hsgr-21ar  ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
 Hsgr-21br  ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
   21acon   ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
   21bcon   ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
    29brc   ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
```

Figure 5 (continued)

```
             1563                                                    1612
     Gdnfr   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
    Hsgr-2   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
    Hsgr-9   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
 Hsgr-21ar   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
 Hsgr-21br   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
    21acon   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
    21bcon   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
     29brc   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT


             1613                                                    1662
     Gdnfr   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
    Hsgr-2   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
    Hsgr-9   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
 Hsgr-21ar   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
 Hsgr-21br   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
    21acon   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
    21bcon   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
     29brc   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC


             1663                                                    1712
     Gdnfr   TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA
    Hsgr-2   TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA
    Hsgr-9   TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA
 Hsgr-21ar   TCTGTCCACC CTATTATCTT TAACAGAAA
 Hsgr-21br   TCTGTCCACC CTATTATTTT TAACAGAAA
    21acon   TCTGTCCACC CTATTATCTT TAACAGAAA
    21bcon   TCTGTCCACC CTATTATCTT TAACAGAAA
     29brc   TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA


             1713                                                    1762
     Gdnfr   ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT
    Hsgr-2   ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT
    Hsgr-9   ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT
     29brc   ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT
```

Figure 5 (continued)

```
        1763                                                    1812
Gdnfr   TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
Hsgr-2  TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
Hsgr-9  TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
29brc   TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT


        1813                                                    1862
Gdnfr   CCATTCAACT GGAACATTTT TTTTTTT.CC TTTTAAGAAA GCTTCTTGTG
Hsgr-2  CCATTCAACT GGAACATTTT TTTTTTT.CC TTTTAAGAAA GCTTCTTGTG
Hsgr-9  CCATTCAACT GGAACATTTT TTTTTTTTCC TTTTAAGAAA GCTTCTTGTG
29brc   CCATTCAACT GGAACATTTT TTTTTTT.CC TTTTAAGAAA GCTTCTTGTG


        1863                                                    1912
Gdnfr   ATCCTTcGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC
Hsgr-2  ATCCTTCGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC
Hsgr-9  ATCCTTTGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC
29brc   ATCCTTCGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC


        1913                                                    1962
Gdnfr   AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG
Hsgr-2  AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG
Hsgr-9  AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG
29brc   AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG


        1963                                                    2012
Gdnfr   CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT cATCATGATc
Hsgr-2  CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC
Hsgr-9  CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT GATCATGATG
29brc   CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC


        2013                                                    2062
Gdnfr   ATGAT..... .......... .......... .......... ....GATTTT
Hsgr-2  ATGAT..... .......... .......... .......... ....GATTTT
Hsgr-9  ATGATCATCA TGATCATGAT GATGATCATC ATGATCATGA TGATGATTTT
29brc   ATGAT..... .......... .......... .......... ....GATTTT
```

Figure 5 (continued)

```
        2063                                                              2112
Gdnfr   AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT

Hsgr-2  AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT

Hsgr-9  AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT

29brc   AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT


        2113                                                              2162
Gdnfr   AAGGTAACTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA

Hsgr-2  AAGGTAACTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA

Hsgr-9  AAGGTAACTC.CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA

29brc   AAGGTAACTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA


        2163                                                              2212
Gdnfr   TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC

Hsgr-2  TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC

Hsgr-9  TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC

29brc   TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC


        2213                                                              2262
Gdnfr   CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA

Hsgr-2  CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA

Hsgr-9  CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA

29brc   CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA


        2263                                                              2312
Gdnfr   TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA

Hsgr-2  TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA

Hsgr-9  TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA

29brc   TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA


        2313                                                              2362
Gdnfr   CTCTTGTACA AAAGAAAAAA CACCTGTCAC ATCCAAATAT AGTATCTGTC

Hsgr-2  CTCTTGTACA AAAGAAAA

Hsgr-9  CTCTTGTACA AAAGAAAA

29brc   CTCTTGTACA AAAGAAAAAA CACCTGTCAC ATCCAAATAT AGTATCTGTC
```

Figure 5 (continued)

```
              2363                                                2412
Gdnfr   TTTTCGTCAA AATAGAGAGT GGGGAATGAG TGTGCCGATT CAATACCTCA
29brc   TTTTCGTCAA AATAGAGAGT GGGGAATGAG TGTGCCGATT CAATACCTCA


              2413                              —                2462
Gdnfr   ATCCCTGAAC GACACTCTCC TAATCCTAAG CCTTACCTGA GTGAGAAGCC
29brc   ATCCCTGAAC GACACTCTCC TAATCCTAAG CCTTACCTGA GTGAGAAGCC


              2463                                                2512
Gdnfr   CTTTACCTAA CAAAAGTCCA ATATAGCTGA AATGTCGCTC TAATACTCTT
29brc   CTTTACCTAA CAAAAGTCCA ATATAGCTGA AATGTCGCTC TAATACTCTT


              2513                                                2562
Gdnfr   TACACATATG AGGTTATATG TAGAAAAAAA TTTTACTACT AAATGATTTC
29brc   TACACATATG AGGTTATATG TAGAAAAAAA TTTTACTACT AAATGATTTC


              2563                                                2612
Gdnfr   AACTATTGGC TTTCTATATT TTGAAAGTAA TGATATTGTC TCATTTTTTT
29brc   AACTATTGGC TTTCTATATT TTGAAAGTAA TGATATTGTC TCATTTTTTT


              2613                     —  .                      2662
Gdnfr   ACTGATGGTT TAATACAAAA TACACAGAGC TTGTTTCCCC TCATAAGTAG
29brc   ACTGATGGTT TAATACAAAA TACACAGAGC TTGTTTCCCC TCATAAGTAG


              2663                                                2712
Gdnfr   TGTTCGCTCT GATATGAACT TCACAAATAC AGCTCATCAA AAGCAGACTC
29brc   TGTTCGCTCT GATATGAACT TCACAAATAC AGCTCATCAA AAGCAGACTC


              2713                                                2762
Gdnfr   TGAGAAGCCT CGTGCTGTAG CAGAAAGTTC TGCATCATGT GACTGTGGAC
29brc   TGAGAAGCCT CGTGCTGTAG CAGAAAGTTC TGCATCATGT GACTGTGGAC


              2763           ··                                   2812
Gdnfr   AGGCAGGAGG AAACAGAACA GACAAGCATT GTCTTTTGTC ATTGCTCGAA
29brc   AGGCAGGAGG AAACAGAACA GACAAGCATT GTCTTTTGTC ATTGCTCGAA
```

Figure 5 (continued)

```
        2813                                                    2862
Gdnfr   GTGCAAGCGT GCATACCTGT GGAGGGAACT GGTGGCTGCT TGTAAATGTT
29brc   GTGCAAGCGT GCATACCTGT GGAGGGAACT GGTGGCTGCT TGTAAATGTT


        2863                                  -               2912
Gdnfr   CTGCAGCATC TCTTGACACA CTTGTCATGA CACAATCCAG TACCTTGGTT
29brc   CTGCAGCATC TCTTGACACA CTTGTCATGA CACAATCCAG TACCTTGGTT


        2913                                                    2962
Gdnfr   TTCAGGTTAT CTGACAAAGG CAGCTTTGAT TGGGACATGG AGGCATGGGC
29brc   TTCAGGTTAT CTGACAAAGG CAGCTTTGAT TGGGACATGG AGGCATGGGC


        2963
Gdnfr   AGGCCGGAA
29brc   AGGCCGGAA
```
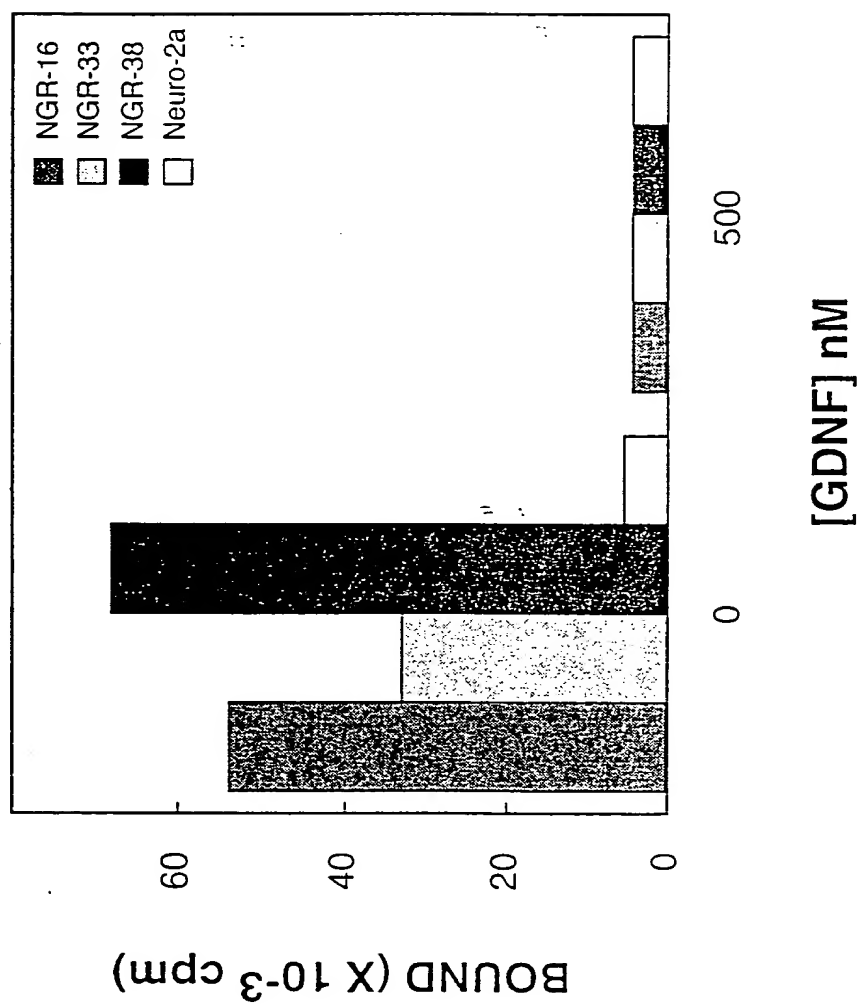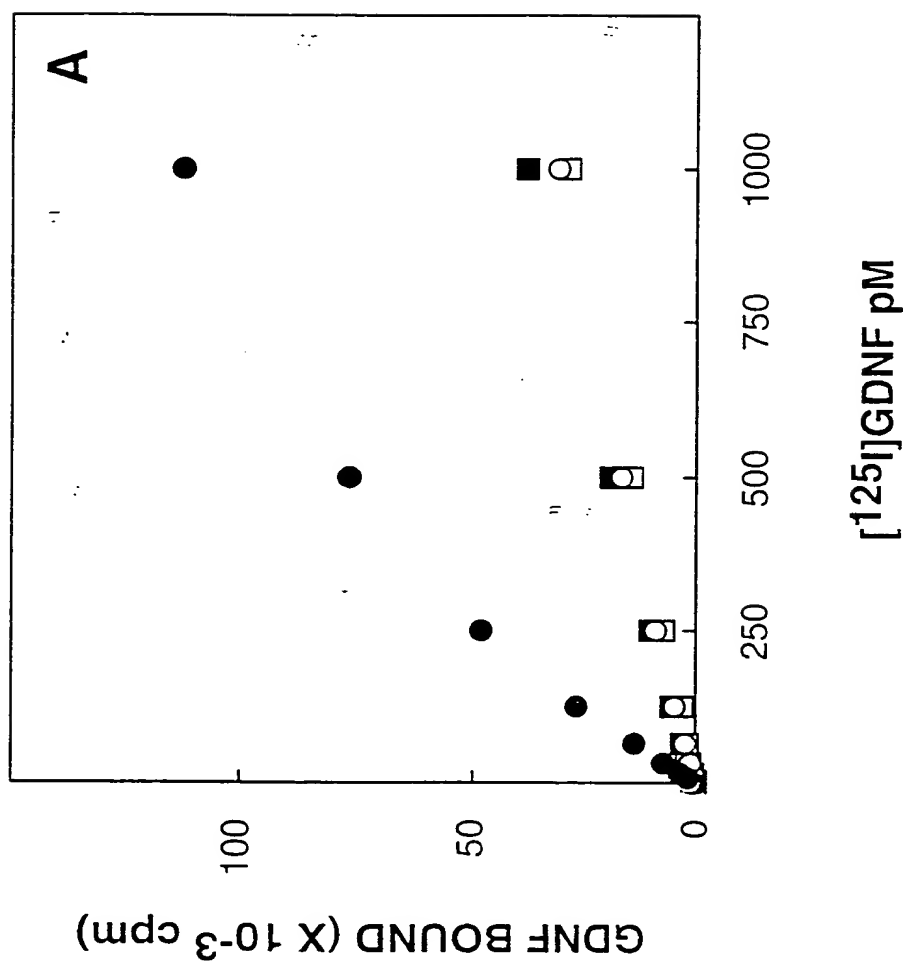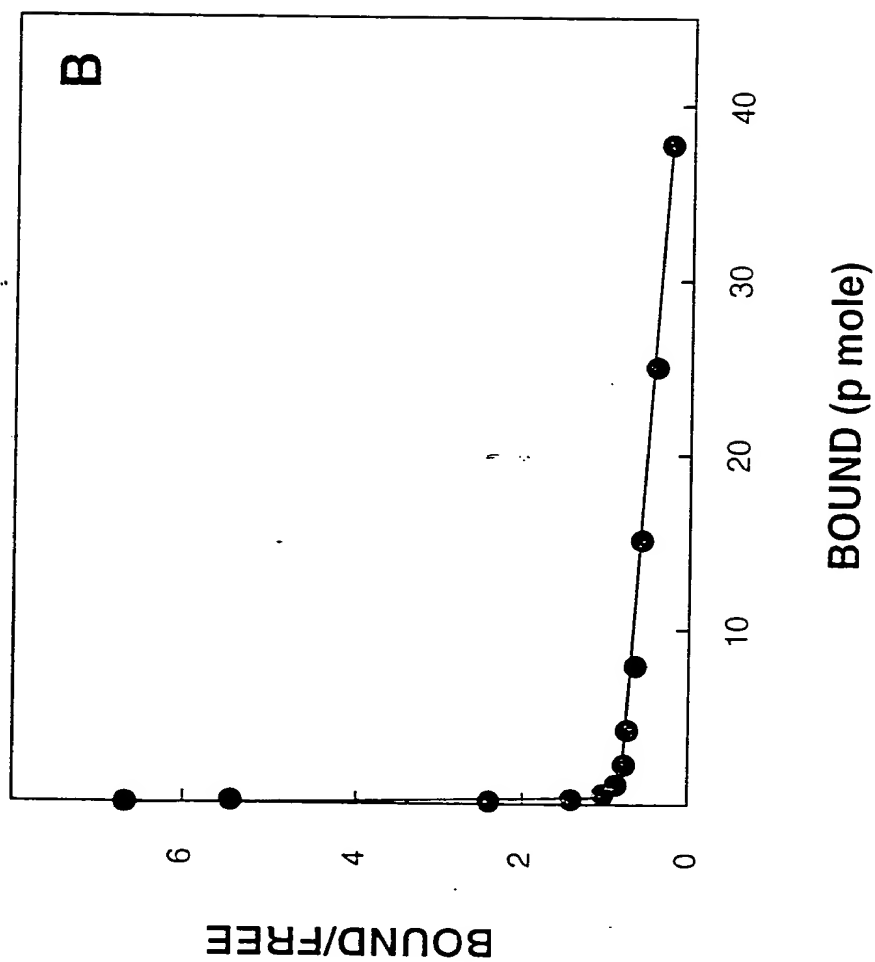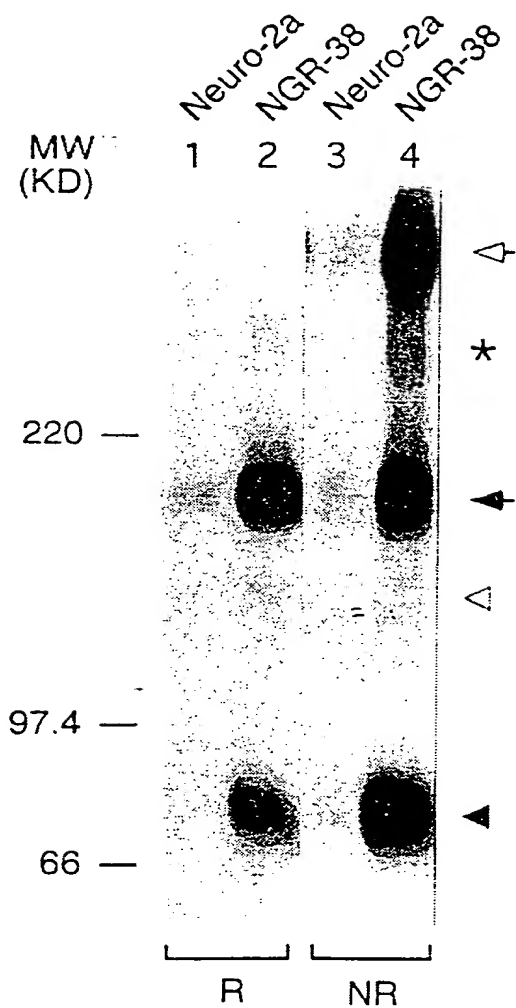
Figure 6

Figure 8

Figure 9A

A

Figure 9B

B

C

Figure 10

A

B
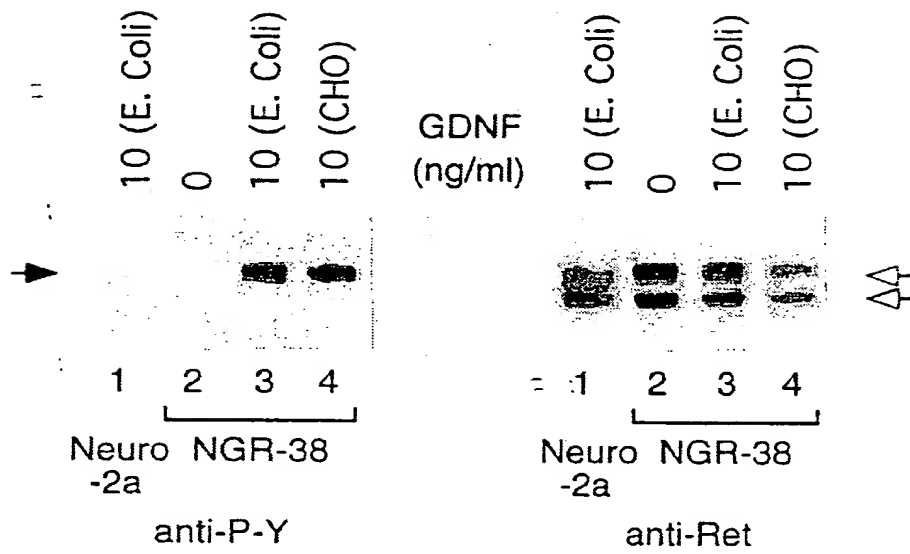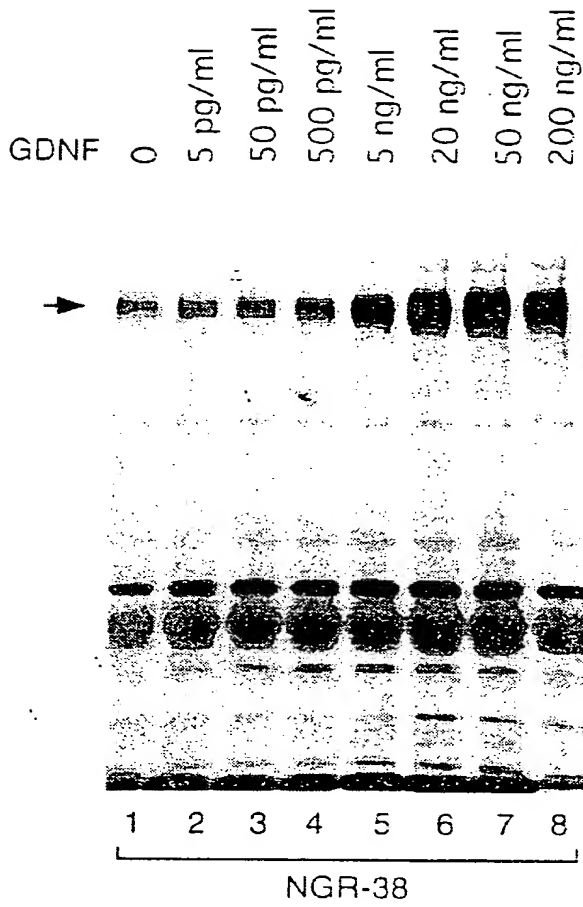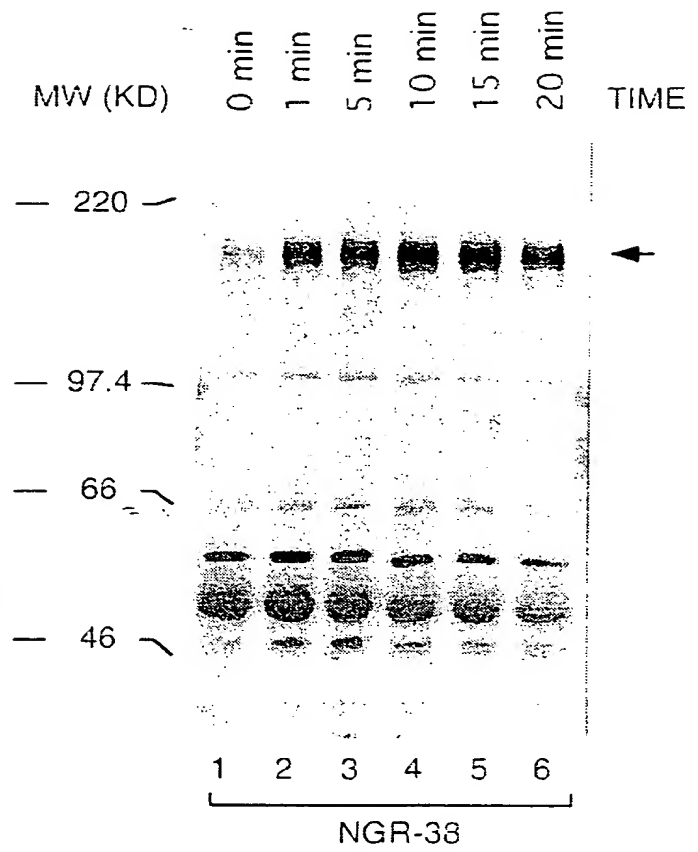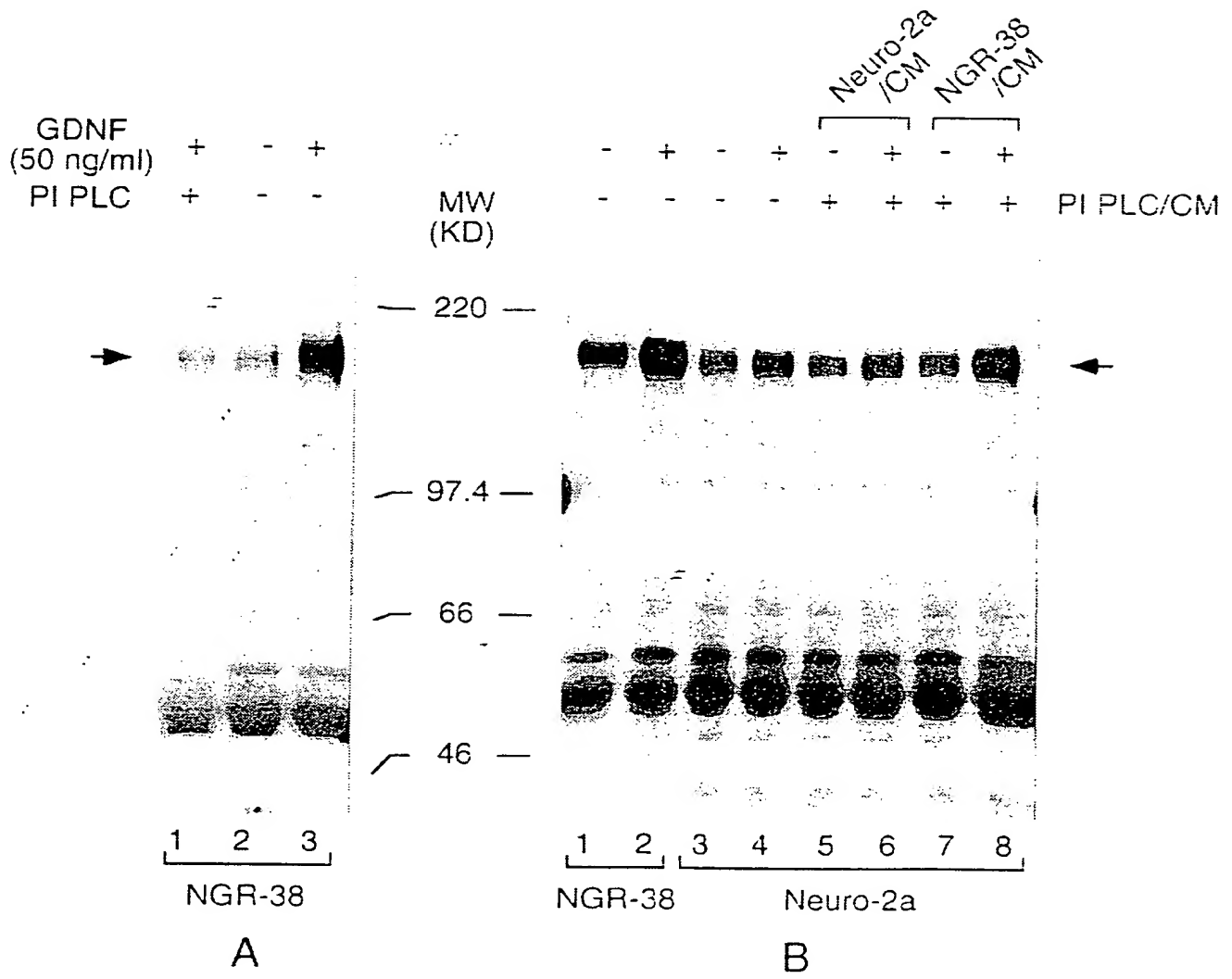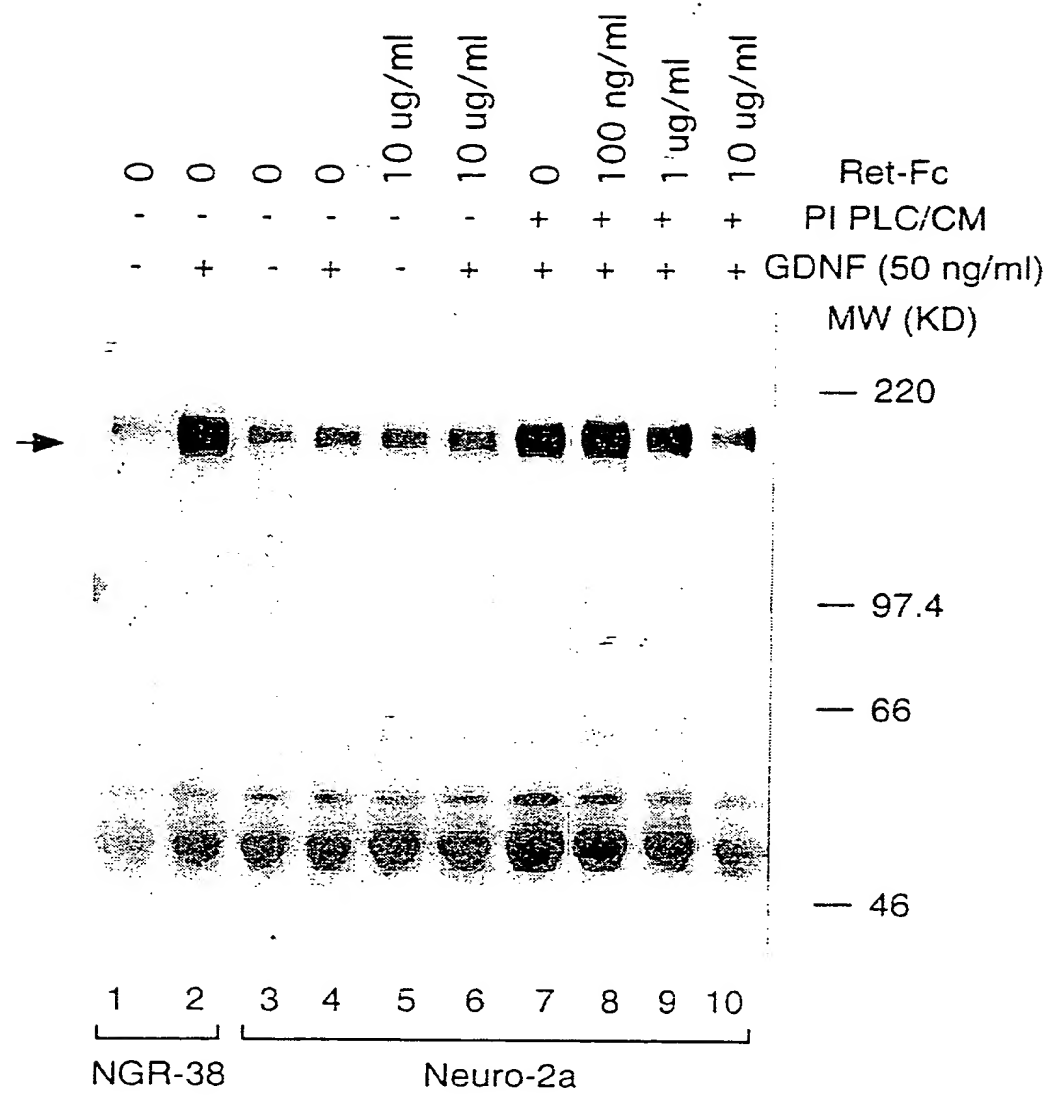
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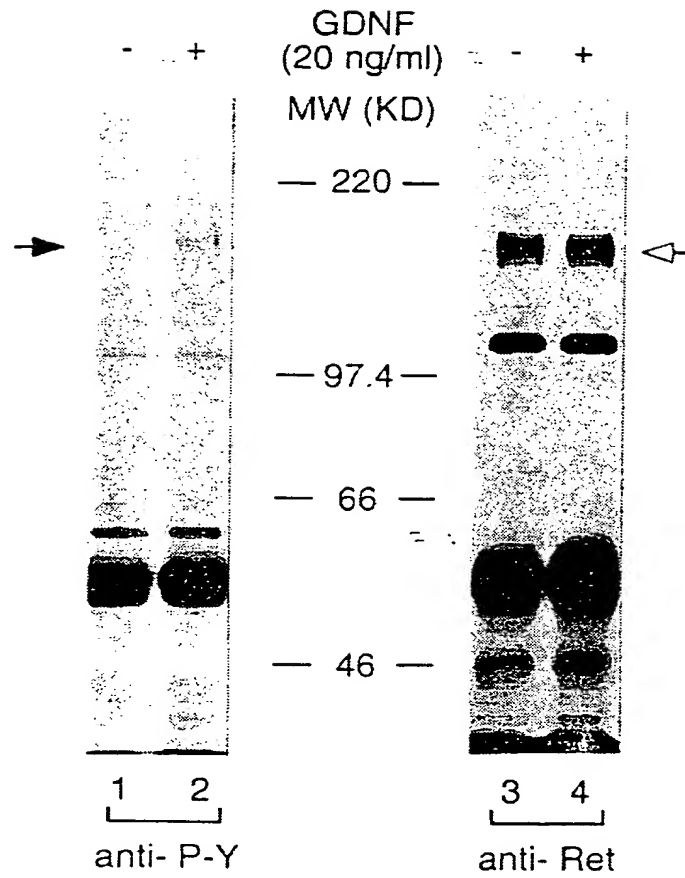
Figure 12

Figure 13

GDNF Signaling Model
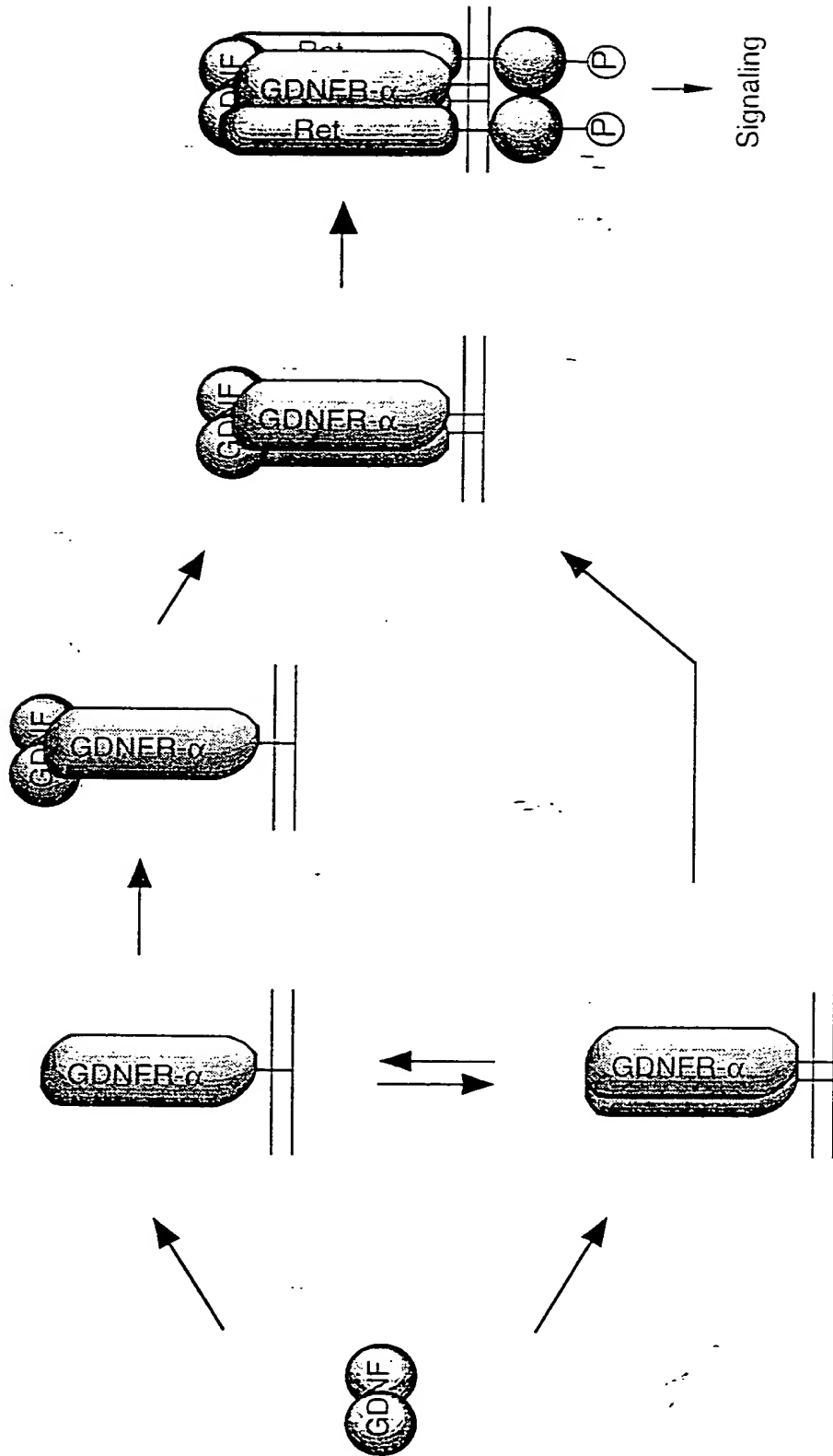
Figure 14

Human GRR2

```
   1  CATGAAGAAACCTCAGTAAGTCTCAGACTTGGCCCAAAGGAGCCCAACTAGTTACTCCCT    60

  61  GGTCTGTTACAGAGGATCTGGCTATTACACTCAACAGCAAAAATTCAATTCAATCCCGCT   120

 121  AAAGATATAAGAATCACTAGGAAKAATAAGCCAGAACTCAAGACAGAAATAGCATTAAGT   180

 181  AGTTCCTTCAGTACAGTGAGCAGAAGCTGGCCACTCTACGACTCTAWAAGACTCAGAAAA   240

 241  GCTTACTAGGGACCWCTGGGCATWCCGGTGTCCTATGTGGGGATTTCGTAACGTCTTTGA   300

 301  GTCAGAAGCTGCCCTCAAAATAGTTTCTTCTCAAAACGGTTTCAGGCTTTGTTAGAAAGG   360

 361  GAAGACTTCACTGCCACTTTACCCAGATCATCTACCCCATCCTTGGAATGAATGGGGAAG   420

 421  CTTCAGCCACCCTACCAGGCTCCTAAAATCACCAACTTGAGAGAAAAACTATAACGTTGC   480

 481  TCTACCAGTACTTCAGGAGGTTAAAGAAAGTCACAGAAGAAAGAACTCTGGGGAAAACA   540

 541  GTCAAATTCGGCTATTAAGACATTAGTTACAGGCCCCTGTACCTCTCCTCTAGAAACCCT   600

 601  GGGAGTACACCCGCAGAGGAGAGAGAGCCCAAGCCACCAAGCAAAGTCAACCAATCTGGC   660

 661  AAAGGGGCGTCCCACTGCGGCTTTCAGTCCAAGAAGTGGATCCTGCTGGTTCGCAGTCTC   720

 721  TCTTCTATCTCCTCACTTCCTATTTACCCTTTGAAGTGGGTACTGAATAGCCCGTTCCCA   780

 781  AGCAGAGGCCCTTTGTATACGGGGTGCTACAGTCGCCTGGTGGAAACACCTTGGCAGAGT   840

 841  TGTTTGGTGCCAGGATGGGCCACTGAAGGCATCTGCTGTGGACACACACACACACACACA   900

 901  CACACACACACACACACAGAGAGAGGAGAGAGAAAGACACACGCACGCAGAGACACAC   960

 961  GGTCACTGGAATTCCATTAGAAAAAAGTGAGCCGAGCAAGGGTTAGCGGGAGAAGATTTT  1020

1021  TTTGAATCTTGTCTTCGTCTTGGTGCGAAAGAAGCGACTCCAGTCTCTCGTCCTCGAAGC  1080

1081  TCCGACTGGATTGTTCTTGGGCGCTGACACCCGTCTGTGGATTTCTTTTCTATTTGCATT  1140
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```
1141  TTATTCCGACCCCCTCCCTCGCCGCTTCCTTCCAGCCCTTCACTCGCAAATCGCCTCTCT  1200


1201  CCCCACCTCCCCAGGCCCCTCCTGGGAAGCGCAGGGGAATTGGACCCGCGGGGACTCACG  1260


1261  CCTTCCCGGACGATTGGAGGGGAGGGCTGACCCCAGGACTGGGCTGTTGGCTTAGAAAGC  1320


1321  CGATACACAGATACGCGTATATTTGATTGTAGCGGGCAAGGGGGGCGTCGAGAGGCAGCA  1380


1381  GCCCATCGCCCGCCTCTCACCCCACCCCCTCCAGCCAGAGGCGAGAATCGCAGGACTCGG  1440


1441  GATCTTCATCGGGTGGACTAGCTGGGATCTCCGCATTGGATTTGGGGCTGATTACCACTG  1500


1501  CTTGGCTATTATTATTGTTGTTGTTACTACTATTATTTTTTTTTACCCAAGGGAGAAAGA  1560


1561  CAAAAAAACGGTGGGATTTATTTAACATGATCTTGGCAAACGTCTTCTGCCTCTTCTTCT  1620
   1                          M   I   L   A   N   V   F   C   L   F   F   F    12


1621  TTCTAGACGACACCCTCCGCTCTTTGGCCAGCCCTTCCTCCCTGCAGGGCCCCGAGCTCC  1680
  13   L   D   D   T   L   R   S   L   A   S   P   S   S   L   Q   G   P   E   L   H    32


1681  ACGGCTGGCGCCCCCCAGTGGACTGTGTCCGGGCCAATGAGCTGTGTGCCGCCGAATCCA  1740
  33   G   W   R   P   P   V   D   C   V   R   A   N   E   L   C   A   A   E   S   N    52


1741  ACTGCAGCTCTCGCTACCGCACTCTGCGGCAGTGCCTGGCAGGCCGCGACCGCAACACCA  1800
  53   C   S   S   R   Y   R   T   L   R   Q   C   L   A   G   R   D   R   N   T   M    72


1801  TGCTGGCCAACAAGGAGTGCCAGGCGGCCTTGGAGGTCTTGCAGGAGAGCCCGCTGTACG  1860
  73   L   A   N   K   E   C   Q   A   A   L   E   V   L   Q   E   S   P   L   Y   D    92


1861  ACTGCCGCTGCAAGCGGGGCATGAAGAAGGAGCTGCAGTGTCTGCAGATCTACTGGAGCA  1920
  93   C   R   C   K   R   G   M   K   K   E   L   Q   C   L   Q   I   Y   W   S   I    112


1921  TCCACCTGGGGCTGACCGAGGGTGAGGAGTTCTACGAAGCCTCCCCCTATGAGCCGGTGA  1980
 113   H   L   G   L   T   E   G   E   E   F   Y   E   A   S   P   Y   E   P   V   T    132


1981  CCTCCCGCCTCTCGGACATCTTCAGGCTTGCTTCAATCTTCTCAGGGACAGGGGCAGACC  2040
 133   S   R   L   S   D   I   F   R   L   A   S   I   F   S   G   T   G   A   D   P    152


2041  CGGTGGTCAGCGCCAAGAGCAACCATTGCCTGGATGCTGCCAAGGCCTGCAACCTGAATG  2100
 153   V   V   S   A   K   S   N   H   C   L   D   A   A   K   A   C   N   L   N   D    172


2101  ACAACTGCAAGAAGCTGCGCTCCTCCTACATCTCCATCTGCAACCGCGAGATCTCGCCCA  2160
 173   N   C   K   K   L   R   S   S   Y   I   S   I   C   N   R   E   I   S   P   T    192
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2161  CCGAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCCAGTTCTTCGACCGGGTGC  2220
193    E   R   C   N   R   R   K   C   H   K   A   L   R   Q   F   F   D   R   V   P    212


2221  CCAGCGAGTACACCTACCGCATGCTCTTCTGCTCCTGCCAAGACCAGGCGTGCGCTGAGC  2280
213    S   E   Y   T   Y   R   M   L   F   C   S   C   Q   D   Q   A   C   A   E   R    232


2281  GCCGCCGGCAAACCATCCTGCCCAGCTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCC  2340
233    R   R   Q   T   I   L   P   S   C   S   Y   E   D   K   E   K   P   N   C   L    252


2341  TGGACCTGCGTGGCGTGTGCCGGACTGACCACCTGTGTCGGTCCCGGCTGGCCGACTTCC  2400
253    D   L   R   G   V   C   R   T   D   H   L   C   R   S   R   L   A   D   F   H    272


2401  ATGCCAATTGTCGAGCCTCCTACCAGACGGTCACCAGCTGCCCTGCGGACAATTACCAGG  2460
273    A   N   C   R   A   S   Y   Q   T   V   T   S   C   P   A   D   N   Y   Q   A    292


2461  CGTGTCTGGGCTCTTATGCTGGCATGATTGGGTTTGACATGACACCTAACTATGTGGACT  2520
293    C   L   G   S   Y   A   G   M   I   G   F   D   M   T   P   N   Y   V   D   S    312


2521  CCAGCCCCACTGGCATCGTGGTGTCCCCCTGGTGCAGCTGTCGTGGCAGCGGGAACATGG  2580
313    S   P   T   G   I   V   V   S   P   W   C   S   C   R   G   S   G   N   M   E    332


2581  AGGAGGAGTGTGAGAAGTTCCTCAGGGACTTCACCGAGAACCCATGCCTCCGGAACGCCA  2640
333    E   E   C   E   K   F   L   R   D   F   T   E   N   P   C   L   R   N   A   I    352


2641  TCCAGGCCTTTGGCAACGGCACGAACGTGAACGTGTCCCCAAAAGGCCCCTCGTTCCAGG  2700
353    Q   A   F   G   N   G   T   N   V   N   V   S   P   K   G   P   S   F   Q   A    372


2701  CCACCCAGGCCCCCTCGGGTGGAGAAGACGCCTTCTTTGCCAGATGACCTCAGTGACAGTA  2760
373    T   Q   A   P   R   V   E   K   T   P   S   L   P   D   D   L   S   D   S   T    392


2761  CCAGCTTGGGGACCAGTGTCATCACCACCTGCACGTCTGTCCAGGAGCAGGGGCTGAAGG  2820
393    S   L   G   T   S   V   I   T   T   C   T   S   V   Q   E   Q   G   L   K   A    412


2821  CCAACAACTCCAAAGAGTTAAGCATGTGCTTCACAGAGCTCACGACAAATATCATCCCAG  2880
413    N   N   S   K   E   L   S   M   C   F   T   E   L   T   T   N   I   I   P   G    432


2881  GGAGTAACAAGGTGATCAAACCTAACTCAGGCCCCAGCAGAGCCAGACCGTCGGCTGCCT  2940
433    S   N   K   V   I   K   P   N   S   G   P   S   R   A   R   P   S   A   A   L    452


2941  TGACCGTGCTGTCTGTCCTGATGCTGAAACTGGCCTTGTAGGCTGTGGGAACCGAGTCAG  3000
453    T   V   L   S   V   L   M   L   K   L   A   L   *    464


3001  AAGATTTTTGAAAGCTACGCAGACAAGAACAGCCGCCTGACGAAATGGAAACACACACAG  3060
```

```
3061  ACACACACACACCTTGCAAAAAAAAAATTGTTTTTCCCACCTTGTCGCTGAACCTGTCTC  3120

3121  CTCCCAGGTTTCTTCTCTGGAGAAGTTTTTGTAAACCAAACAGACAAGCAGGCAGGCAGC  3180

3181  CTGAGAGCTGGCCCAGGGGTCCCCTGGCAGGGGAAACTCTGGTGCCGGGGAGGGCACGAG  3240

3241  GCTCTAGAAATGCCCTTCACTTTCTCCTGGTGTTTTTCTCTCTGGACCCTTCTGAAGCAG  3300

3301  AGACCGGACAAGAGCCTGCAGCGGAAGGGACTCTGGGCTGTGCCTGAGGCTGGCTGGGGG  3360

3361  CAGGACAACACAGCTGCTTCCCCAGGCTGCCCACTCTGGGGACCCGCTGGGGGCTGGCAG  3420

3421  AGGGCATCGGTCAGCGGGGCAGCGGGGCTGGCCATGAGGGTCCACCTTCAGCCCTTTGGC  3480

3481  TTCAAGGATGGAGATGGTTTTGCCCTCCCTCTCTGCCCTCGGGTGGGGCTGGTGGGTCTG  3540

3541  CAGCTGGTGTGGGAACTTCCCCACGGATGGCGGTGGAGGGGGTTCGCACCGTGCTGGGCT  3600

3601  CCCCCTGACTGTAGCACGGAGTGTTGGGGCTGGGGGCCAGCTCCAGGAGGGCTTGAGAGC  3660

3661  TCAGCCTGCCTGGGAGAGCCCTTGTGGCGAGGCATTAAAACTTGGGCACCAGCTTCTTTC  3720

3721  TCGGTGGCAGAAATTTTGAAGTCAGAGAGAAACGGTCCTTTGTTGGCTTCTTTGCTTTCT  3780

3781  CGTGGGTCCTTTGGCAGGCCTCCCTTTGGGGAGAGGGAGGGGAGAGACCACAGCCGGGTG  3840

3841  TGTGTCTGCAGCACCGTGGGCCCTCAAGCTTTCCTGCTGTCTTCTCCCTCCTCCTCCTTT  3900

3901  CCCCTTTCTCTTTCCTCATTTCCTAGACGTACGTCAACTGTATGTACATACCGGGGCTCC  3960

3961  TCTCCTAACATATATGTATATACACATCCATATACATATATTGTGTGGTTTCCCCTTTCT  4020

4021  TTCCTTTTTTTAAGCAACAAAACTATGGAAATAATACCCCAACAGATGAGCGAAAATGTA  4080

4081  TTATTGTAAAGTTTATTTTTTTTAATACTGTTGTCTATAATGGGGAAAAAGGACATTGGC  4140

4141  CCCGCAGTGCCCTGCCCCAGTCAGCCTGGCTGGGCTCTGGTGGGGGCTCCTGATCCGCAT  4200

4201  CCAAGCTTAACCAAGGCTCCAATAAACGTGCG  4232
```

Figure 15

Human GRR3

```
  1   CAAGTCAAAGGTTTAATCATGATCCAAGAGCCCAGAGAGACTTTAGGACAATAATAGGAA      60


 61   TAAAGCAAGGCCCACAGGCTCCAGCTCCTGATGCCCAGATGTTCGGCAGGATCCGGGGAC     120


121   AGGGCAGTGCAGGCAGTAGTTTTCCATCCTCCATCCAGGGGAGGAGCGAGGGGAGCGCGG     180


181   AGCCCGGCGCCTACAGCTCGCCATGGTGCGCCCCCTGAACCCGCGACCGCTGCCGCCCGT     240
  1                           M   V   R   P   L   N   P   R   P   L   P   P   V     13


241   AGTCCTGATGTTGCTGCTGCTGCCGCCGTCGCCGCTGCCTCTCGCAGCCGGAGACCC      300
 14    V   L   M   L   L   L   L   P   P   S   P   L   P   L   A   A   G   D   P     33


301   CCTTCCCACAGAAAGCCGACTCATGAACAGCTGTCTCCAGGCCAGGAGGAAGTGCCAGGC     360
 34    L   P   T   E   S   R   L   M   N   S   C   L   Q   A   R   R   K   C   Q   A     53


361   TGATCCCACCTGCAGTGCTGCCTACCACCACCTGGATTCCTGCACCTCTAGCATAAGCAC     420
 54    D   P   T   C   S   A   A   Y   H   H   L   D   S   C   T   S   S   I   S   T     73


421   CCCACTGCCCTCAGAGGAGCCTTCGGTCCCTGCTGACTGCCTGGAGGCAGCACAGCAACT     480
 74    P   L   P   S   E   E   P   S   V   P   A   D   C   L   E   A   A   Q   Q   L     93


481   CAGGAACAGCTCTCTGATAGGCTGCATGTGCCACCGGCGCATGAAGAACCAGGTTGCCTG     540
 94    R   N   S   S   L   I   G   C   M   C   H   R   R   M   K   N   Q   V   A   C     113


541   CTTGGACATCTATTGGACCGTTCACCGTGCCCGCAGCCTTGGTAACTATGAGCTGGATGT     600
114    L   D   I   Y   W   T   V   H   R   A   R   S   L   G   N   Y   E   L   D   V     133


601   CTCCCCCTATGAAGACACAGTGACCAGCAAACCCTGGAAAATGAATCTCAGCAAACTGAA     660
134    S   P   Y   E   D   T   V   T   S   K   P   W   K   M   N   L   S   K   L   N     153


661   CATGCTCAAACCAGACTCAGACCTCTGCCTCAAGTTTGCCATGCTGTGTACTCTCAATGA     720
154    M   L   K   P   D   S   D   L   C   L   K   F   A   M   L   C   T   L   N   D     173


721   CAAGTGTGACCGGCTGCGCAAGGCCTACGGGGAGGCGTGCTCCGGGCCCCACTGCCAGCG     780
174    K   C   D   R   L   R   K   A   Y   G   E   A   C   S   G   P   H   C   Q   R     193


781   CCACGTCTGCCTCAGGCAGCTGCTCACTTTCTTCGAGAAGGCCGCCGAGCCCCACGCGCA     840
194    H   V   C   L   R   Q   L   L   T   F   F   E   K   A   A   E   P   H   A   Q     213


841   GGGCCTGCTACTGTGCCCATGTGCCCCCAACGACCGGGGCTGCGGGGAGCGCCGGCGCAA     900
214    G   L   L   L   C   P   C   A   P   N   D   R   G   C   G   E   R   R   R   N     233
```

```
901  CACCATCGCCCCCAACTGCGCGCTGCCGCCTGTGGCCCCCAACTGCCTGGAGCTGCGGCG  960
234    T   I   A   P   N   C   A   L   P   P   V   A   P   N   C   L   E   L   R   R   253

961  CCTCTGCTTCTCCGACCCGCTTTGCAGATCACGCCTGGTGGATTTCCAGACCCACTGCCA  1020
254    L   C   F   S   D   P   L   C   R   S   R   L   V   D   F   Q   T   H   C   H   273

1021 TCCCATGGACATCCTAGGAACTTGTGCAACAGAGCAGTCCAGATGTCTACGAGCATACCT  1080
274    P   M   D   I   L   G   T   C   A   T   E   Q   S   R   C   L   R   A   Y   L   293

1081 GGGGCTGATTGGGACTGCCATGACCCCCAACTTTGCCAGCAATGTCAACACCAGTGTTGC  1140
294    G   L   I   G   T   A   M   T   P   N   F   A   S   N   V   N   T   S   V   A   313

1141 CTTAAGCTGCACCTGCCGAGGCAGTGGCAACCTGCAGGAGGAGTGTGAAATGCTGGAAGG  1200
314    L   S   C   T   C   R   G   S   G   N   L   Q   E   E   C   E   M   L   E   G   333

1201 GTTCTTCTCCCACAACCCCTGCCTCACGGAGGCCATTGCAGCTAAGATGCGTTTTCACAG  1260
334    F   F   S   H   N   P   C   L   T   E   A   I   A   A   K   M   R   F   H   S   353

1261 CCAACTCTTCTCCCAGGACTGGCCACACCCTACCTTTGCTGTGATGGCACACCAGAATGA  1320
354    Q   L   F   S   Q   D   W   P   H   P   T   F   A   V   M   A   H   Q   N   E   373

1321 AAACCCTGCTGTGAGGCCACAGCCCTGGGTGCCCTCTCTTTTCTCCTGCACGCTTCCCTT  1380
374    N   P   A   V   R   P   Q   P   W   V   P   S   L   F   S   C   T   L   P   L   393

1381 GATTCTGCTCCTGAGCCTATGGTAGCTGGACTTCCCCAGGGCCCTCTTCCCCTCCACCAC  1440
394    I   L   L   L   S   L   W   *   400

1441 ACCCAGGTGGACTTGCAGCCCACAAGGGGTGAGGAAAGGACAGCAGCAGGAAGGAGGTGC  1500

1501 AGTGCGCAGATGAGGGCACAGGAGAAGCTAAGGGTTATGACCTCCAGATCCTTACTGGTC  1560

1561 CAGTCCTCATTCCCTCCACCCCATCTCCACTTCTGATTCATGCTGCCCCTCCTTGGTGGC  1620

1621 CACAATTTAGCCATGTCATCTGGTGGTGACCAGCTCCACCAAGCCCCTTTGTGAGCCCTT  1680

1681 CCTCTTGACTACCAGGATCACCAGAATCTAATAAGTTAGCCTTTCTCTATTGCATTCCAG  1740

1741 ATTAGGGTTAGGGTAGGGAGGACTGGGTGTTCTGAGGCAGCCTAGAAAGTCATTCTCCTT  1800

1801 TGTGAAGAAGGCTCCTGCCCCCTCGTCTCCTCCTCTGAGTGGAGGATGGAAAACTACTGC  1860

1861 CTGCACTGCCCTGTCCCCGGATCCTGCCGAACATCTGGGCATCAGGAGCTGGAGCCTGTG  1920
```

1921   GGCCTTGCTTTATTCCTATTATTGTCCTAAAGTCTCTCTGGGCTCTTGGATCATGATTAA   1980

1981   ACCTTTGACTG   1991

Figure 16

Rat GRR2

```
    1  GCGGCCGCGTCGACCTTGACCATGCAGACACTTTTTCAGGCCTCTGTCTGGTGTGAAGTT       60

   61  GGCAGATACAAGCAAGGCCCGAAAGGGGTCTCAGCTTCTCTCTCCTGGGCCTCCTGGACT      120

  121  GAGTTAGGCTTGCTTCTGGTTGTCTTCTAAAGGCACGGTGATACAGAATGATGAGACTAG      180

  181  GCTGGAGGGGGCTTTCTGCTTCTCTGTGTGTGACCTTGAGTTATCTCCCTTCGTTGGATC      240

  241  CGAGCTTTCCTGGAATATGATGTTGAATATGAATATGAGTTCTGCCTAAGGTCCAGACAG      300

  301  GCTCTGAGGGTTAACTGACTTTTGGAGCCTTCAAATCAATACCTTGGATGGAGTGGGGGT      360

  361  TTGTCCAATGGGAGTTGAGGCAAGATCCCTTTGCATAAGCCTTGCCACATCATGTTGAAG      420

  421  CCATGCCATTCTGTCTGGACTATTGGCATCTTACCTTTCCAGCAGTTTCAGTGAAGGCCT      480

  481  TCCTGGATTTATCATTCTGTGTTCCACTGCCTAGGATTGTGCTCAAGAGGAAATGAATGT      540

  541  GAACCATGGTTGTAGGGGAGTATGGCCAACCAGGTTGGGTCTGTGTTGACCTTGGTCTTG      600
    1        M   V   V   G   E   Y   G   Q   P   G   W   V   C   V   D   L   G   L   G       19

  601  GTGTTCTTTTGTGTAAAGTGGGTGAGAAGTTCCTTCAAACCTTAGGCCTACATTGGGGTC      660
   20        V   L   L   C   K   V   G   E   K   F   L   Q   T   L   G   L   H   W   G   Q       39

  661  AGAGACTGTGGTGGCCCTCATTCATGCTTGTCTTCCCTTCCCACTACCCAGACGAAACCC      720
   40        R   L   W   W   P   S   F   M   L   V   F   P   S   H   Y   P   D   E   T   L       59

  721  TCCGCTCTTTGGCCAGCCCTTCCTCCCTGCAGGGCTCTGAGCTCCACGGCTGGCGCCCCC      780
   60        R   S   L   A   S   P   S   S   L   Q   G   S   E   L   H   G   W   R   P   Q       79

  781  AAGTGGACTGTGTCCGGGCCAATGAGCTGTGTGCGGCTGAATCCAACTGCAGCTCCAGGT      840
   80        V   D   C   V   R   A   N   E   L   C   A   A   E   S   N   C   S   S   R   Y       99

  841  ACCGCACCCTTCGGCAGTGCCTGGCAGGCCGGGATCGCAATACCATGCTGGCCAATAAGG      900
  100        R   T   L   R   Q   C   L   A   G   R   D   R   N   T   M   L   A   N   K   E      119

  901  AGTGCCAGGCAGCCCTGGAGGTCTTGCAGGAAAGCCCACTGTATGACTGCCGCTGCAAGC      960
  120        C   Q   A   A   L   E   V   L   Q   E   S   P   L   Y   D   C   R   C   K   R      139
```

```
 961  GGGGCATGAAGAAGGAGCTGCAGTGTCTGCAGATCTACTGGAGCATCCATCTGGGGCTGA  1020
 140     G   M   K   K   E   L   Q   C   L   Q   I   Y   W   S   I   H   L   G   L   T   159

1021  CAGAGGGTGAGGAGTTCTATGAAGCTTCCCCCTATGAGCCTGTGACCTCGCGCCTCTCGG  1080
 160     E   G   E   E   F   Y   E   A   S   P   Y   E   P   V   T   S   R   L   S   D   179

1081  ACATCTTCAGGCTCGCTTCAATCTTCTCAGGGACAGGGACAGACCCGGCGGTCAGTACCA  1140
 180     I   F   R   L   A   S   I   F   S   G   T   G   T   D   P   A   V   S   T   K   199

1141  AAAGCAACCACTGCCTGGATGCCGCCAAGGCCTGCAACCTGAATGACAACTGCAAGAAGC  1200
 200     S   N   H   C   L   D   A   A   K   A   C   N   L   N   D   N   C   K   K   L   219

1201  TTCGCTCCTCTTATATCTCCATCTGCAACCGTGAGATCTCTCCCACCGAACGCTGCAACC  1260
 220     R   S   S   Y   I   S   I   C   N   R   E   I   S   P   T   E   R   C   N   R   239

1261  GCCGCAAGTGCCACAAGGCTCTGCGCCAGTTCTTTGACCGTGTGCCCAGCGAGTATACCT  1320
 240     R   K   C   H   K   A   L   R   Q   F   F   D   R   V   P   S   E   Y   T   Y   259

1321  ACCGCATGCTCTTCTGCTCCTGTCAGGACCAGGCATGTGCTGAGCGTCGCCGGCAAACCA  1380
 260     R   M   L   F   C   S   C   Q   D   Q   A   C   A   E   R   R   R   Q   T   I   279

1381  TCCTGCCCAGTTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCCTGGACCTGCGCAGCC  1440
 280     L   P   S   C   S   Y   E   D   K   E   K   P   N   C   L   D   L   R   S   L   299

1441  TGTGTCGTACAGACCACCTGTGCCGGTCCCGACTGGCAGATTTCCACGCCAACTGTCGAG  1500
 300     C   R   T   D   H   L   C   R   S   R   L   A   D   F   H   A   N   C   R   A   319

1501  CCTCCTACCGGACAATCACCAGCTGTCCTGCGGACAACTACCAGGCATGTCTGGGCTCCT  1560
 320     S   Y   R   T   I   T   S   C   P   A   D   N   Y   Q   A   C   L   G   S   Y   339

1561  ATGCTGGCATGATTGGGTTTGATATGACACCCAACTATGTGGACTCCAACCCCACGGGCA  1620
 340     A   G   M   I   G   F   D   M   T   P   N   Y   V   D   S   N   P   T   G   I   359

1621  TCGTGGTGTCTCCCTGGTGCAATTGTCGTGGCAGTGGGAACATGGAAGAAGAGTGTGAGA  1680
 360     V   V   S   P   W   C   N   C   R   G   S   G   N   M   E   E   E   C   E   K   379

1681  AGTTCCTCAGGGACTTCACGGAAAACCCATGCCTCCGGAATGCCATTCAGGCCTTTGGTA  1740
 380     F   L   R   D   F   T   E   N   P   C   L   R   N   A   I   Q   A   F   G   N   399

1741  ATGGCACAGATGTGAACATGTCTCCCAAAGGCCCCTCACTCCCAGCTACCCAGGCCCCTC  1800
 400     G   T   D   V   N   M   S   P   K   G   P   S   L   P   A   T   Q   A   P   R   419

1801  GGGTGGAGAAGACTCCTTCACTGCCAGATGACCTCAGTGACAGCACCAGCCTGGGGACCA  1860
 420     V   E   K   T   P   S   L   P   D   D   L   S   D   S   T   S   L   G   T   S   439

1861  GTGTCATCACCACCTGCACATCTATCCAGGAGCAAGGGCTGAAGGCCAACAACTCCAAAG  1920
```

```
440      V   I   T   T   C   T   S   I   Q   E   Q   G   L   K   A   N   N   S   K   E      459


1921   AGTTAAGCATGTGCTTCACAGAGCTCACGACAAACATCAGTCCAGGGAGTAAAAAGGTGA   1980
460      L   S   M   C   F   T   E   L   T   T   N   I   S   P   G   S   K   K   V   I      479


1981   TCAAACTTAACTCAGGCTCCAGCAGAGCCAGACTGTCGGCTGCCTTGACTGCCCTCCCAC   2040
480      K   L   N   S   G   S   S   R   A   R   L   S   A   A   L   T   A   L   P   L      499


2041   TCCTGATGCTGACCTTGGCCTTGTAGGCCTTTGGAACCCAGCACAAAAGTTCTTCAAGCA   2100
500      L   M   L   T   L   A   L   *                                                    506


2101   ACCCAGATATGAACTCCCGCCTGACAAAATGGAAACACACGCATACACACATGCCACACA   2160


2161   CAGACACACACACAGACACACACACACACACACATACAGACGTCGACGCGGCCGC   2215
```

Figure 17

Rat GRR3

```
   1  GCGGCCGCGTCGACCGACGCCCAGCACAGGCAGAGCGCTGCCGGGTCCGCGGCGTCCAGA    60


  61  CCCGCCATGGGGCTCTCCCGGAGCCCGCGACCGCCGCCGCTAGTGATCCTGCTACTGGTG   120
   1        M   G   L   S   R   S   P   R   P   P   P   L   V   I   L   L   L   V    18


 121  CTGTCGCTGTGGCTACCCCTTGGAACAGGAAACTCCCTTCCCACAGAGAACAGGCTTGTG   180
  19   L   S   L   W   L   P   L   G   T   G   N   S   L   P   T   E   N   R   L   V    38


 181  AACAGCTGTACCCAGGCCAGAAAAAAATGCGAGGCTAATCCCGCTTGCAAGGCTGCCTAC   240
  39   N   S   C   T   Q   A   R   K   K   C   E   A   N   P   A   C   K   A   A   Y    58


 241  CAGCACCTGGACTCCTGCACCCCCAGTCTCAGCAGTCCACTGCCCTCAGGGGAGTCTGCC   300
  59   Q   H   L   D   S   C   T   P   S   L   S   S   P   L   P   S   G   E   S   A    78


 301  ACATCTGCAGCGTGCCTTGAAGCAGCACAGCAACTCAGGAACAGCTCTCTCATAGACTGC   360
  79   T   S   A   A   C   L   E   A   A   Q   Q   L   R   N   S   S   L   I   D   C    98


 361  AGGTGCCACCGGCGCATGAAGCACCAAGCTACCTGTCTGGACATTTATTGGACCGTTCAC   420
  99   R   C   H   R   R   M   K   H   Q   A   T   C   L   D   I   Y   W   T   V   H   118


 421  CCTGTCCGAAGCCTTGGTGACTACGAGTTGGACGTCTCACCCTATGAAGACACAGTGACC   480
 119   P   V   R   S   L   G   D   Y   E   L   D   V   S   P   Y   E   D   T   V   T   138


 481  AGCAAACCCTGGAAAATGAATCTCAGCAAGCTGAGCATGCTCAAACCAGACTCCGACCTC   540
 139   S   K   P   W   K   M   N   L   S   K   L   S   M   L   K   P   D   S   D   L   158


 541  TGCCTCAAATTTGCTATGCTGTGTACTCTTAACGACAAGTGCGACCGCCTCCGAAAGGCC   600
 159   C   L   K   F   A   M   L   C   T   L   N   D   K   C   D   R   L   R   K   A   178


 601  TACGGGGAGGCGTGCTCAGGGATCCGCTGCCAGCGCCACCTCTGCCTAGCTCAGCTGCGC   660
 179   Y   G   E   A   C   S   G   I   R   C   Q   R   H   L   C   L   A   Q   L   R   198


 661  TCCTTCTTCGAGAAGGCGGCAGAGTCCCACGCTCAGGGCCTGCTGCTGTGTCCCTGTGCA   720
 199   S   F   F   E   K   A   A   E   S   H   A   Q   G   L   L   L   C   P   C   A   218


 721  CCCGAAGATGCGGGCTGTGGGGAGCGCCGGCGCAACACCATCGCCCCCAGTTGCGCCCTC   780
 219   P   E   D   A   G   C   G   E   R   R   R   N   T   I   A   P   S   C   A   L   238


 781  CCGTCTGTGGCCCCCAACTGCCTAGATCTTCGGAGCTTCTGCCGTGCGGACCCTCTGTGC   840
 239   P   S   V   A   P   N   C   L   D   L   R   S   F   C   R   A   D   P   L   C   258
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```
 841  AGATCACGCCTGATGGACTTCCAGACCCACTGCCACCCTATGGACATCCTCGGGACTTGT   900
 259   R   S   R   L   M   D   F   Q   T   H   C   H   P   M   D   I   L   G   T   C    278

 901  GCAACTGAGCAGTCCAGATGTCTGCGGGCATACCTGGGGCTAATTGGGACTGCCATGACC   960
 279   A   T   E   Q   S   R   C   L   R   A   Y   L   G   L   I   G   T   A   M   T    298

 961  CCAAACTTCATCAGCAAGGTCAACACTACTGTTGCCTTAGGCTGTACCTGCCGAGGCAGT  1020
 299   P   N   F   I   S   K   V   N   T   T   V   A   L   G   C   T   C   R   G   S    318

1021  GGCAACCTGCAGGACGAGTGTGAACAGCTGGAAAAGTCCTTCTCCCAGAACCCCTGCCTC  1080
 319   G   N   L   Q   D   E   C   E   Q   L   E   K   S   F   S   Q   N   P   C   L    338

1081  ATGGAGGCCATTGCGGCTAAAATGCGTTTCCACAGACAACTCTTCTCCCAGGACTGGGCG  1140
 339   M   E   A   I   A   A   K   M   R   F   H   R   Q   L   F   S   Q   D   W   A    358

1141  GACTCTACTTTTTCTGTGATGCAGCAGCAGAACAGCAGCCCTGCTCTGAGGCCCCAGCTC  1200
 359   D   S   T   F   S   V   M   Q   Q   Q   N   S   S   P   A   L   R   P   Q   L    378

1201  AGGCTACCCGTTCTGTCTTTCTTCATCCTTACCTTGATTCTGCTGCAGACCCTCTGGTAA  1260
 379   R   L   P   V   L   S   F   F   I   L   T   L   I   L   L   Q   T   L   W   *    397

1261  CTGGGCTCCCTCAGGGTCCTTTGTCCTCTCCACCACACCCAGACCGACTTGCAGCCTGTG  1320

1321  ATGGGAGAGAAAATGCTGGCCTCTGGAAGAAGATGCAACCAGGCTCACTGCACATCCTGT  1380

1381  CTGCTCCAGATGAGGTCTTGGAAGAAGCGAGGGCTGTGACCGTTCAGAATCCTGAGCGGC  1440

1441  CAGCTTTCAAACCTCTCCTACTTACTCCTGCTTGGGCTGCTCCTCCCTAGGACCTTGTAC  1500

1501  TCCAGTTTGGCTGTATATTGTGGTGGTGATTAGCTTCCCACCTCCAGCCCTTCTTCCTGT  1560

1561  TTCCCAGGACCACCCAGGGCTAATGACTCACTCATTCCTGGTTGCCTTCTCCAGGAAGGC  1620

1621  AGGCTGAGGGTTCTGAGGCAGCTGAGAAAGATGGTCCCTTTGTGAGGAAGGCTGGTGGTC  1680

1681  CAACCGTCGACGCGGCCGC   1699
```

Figure 18

Alignment of the Amino Acid Sequeces of GDNFRs

```
1                                                         50
Mgdnfr   ~~~~~~~~~~   ~~~~MFLATL   YFVLPLLDLL   MSAEVSG.GD   RLDCVKASDQ

Rgdnfr   ~~~~~~~~~~   ~~~~MFLATL   YFALPLLDLL   MSAEVSG.GD   RLDCVKASDQ

Hgdnfr   ~~~~~~~~~~   ~~~~MFLATL   YFALPLLDLL   LSAEVSG.GD   RLDCVKASDQ

 Hgrr2   ~~~~MILANV   FCLFFFLDDT   LRSLASPSSL   QGPELHGWRP   PVDCVRANEL

 Rgrr2   ~~~~~~~~ML   VFPSHYPDET   LRSLASPSSL   QGSELHGWRP   QVDCVRANEL

 Hgrr3   MVRPLNPRPL   PPVVLMLLLL   LPPSPLPLAA   GDPLPTESRL   MNSCLQARRK

 Rgrr3   MGLSRSPRPP   PLVILLLVLS   L...WLPLGT   GNSLPTENRL   VNSCTQARKK


51                                                        100
Mgdnfr   CLKEQSCSTK   YRTLRQCVAG   KETNFSLTSG   LEAKDECRSA   MEALKQKSLY

Rgdnfr   CLKEQSCSTK   YRTLRQCVAG   KETNFSLTSG   LEAKDECRSA   MEALKQKSLY

Hgdnfr   CLKEQSCSTK   YRTLRQCVAG   KETNFSLASG   LEAKDECRSA   MEALKQKSLY

 Hgrr2   CAAESNCSSR   YRTLRQCLAG   RDRNTML...   ..ANKECQAA   LEVLQESPLY

 Rgrr2   CAAESNCSSR   YRTLRQCLAG   RDRNTML...   ..ANKECQAA   LEVLQESPLY

 Hgrr3   CQADPTCSAA   YHHLDSCTSS   ISTPLP.SEE   PSVPADCLEA   AQQLRNSSLI

 Rgrr3   CEANPACKAA   YQHLDSCTPS   LSSPLP.SGE   SATSAACLEA   AQQLRNSSLI


101                                                       150
Mgdnfr   NCRCKRGMKK   EKNCLRIYWS   MYQSL.QGND   LLEDSPYEPV   NSRLSDIFRA

Rgdnfr   NCRCKRGMKK   EKNCLRIYWS   MYQSL.QGND   LLEDSPYEPV   NSRLSDIFRA

Hgdnfr   NCRCKRGMKK   EKNCLRIYWS   MYQSL.QGND   LLEDSPYEPV   NSRLSDIFRV

 Hgrr2   DCRCKRGMKK   ELQCLQIYWS   IHLGLTEGEE   FYEASPYEPV   TSRLSDIFRL

 Rgrr2   DCRCKRGMKK   ELQCLQIYWS   IHLGLTEGEE   FYEASPYEPV   TSRLSDIFRL

 Hgrr3   GCMCHRRMKN   QVACLDIYWT   VHRARSLGNY   ELDVSPYE..   .....DTVTS

 Rgrr3   DCRCHRRMKH   QATCLDIYWT   VHPVRSLGDY   ELDVSPYE..   .....DTVTS


151                                                       200
Mgdnfr   VPFISDVFQQ   VEHISKGNNC   LDAAKACNLD   DTCKKYRSAY   ITPCTTSMS.

Rgdnfr   VPFISDVFQQ   VEHISKGNNC   LDAAKACNLD   DTCKKYRSAY   ITPCTTSMS.

Hgdnfr   VPFISDVFQQ   VEHIPKGNNC   LDAAKACNLD   DICKKYRSAY   ITPCTTSVS.

 Hgrr2   ASIFSGTGAD   PVVSAKSNHC   LDAAKACNLN   DNCKKLRSSY   ISICNREISP

 Rgrr2   ASIFSGTGTD   PAVSTKSNHC   LDAAKACNLN   DNCKKLRSSY   ISICNREISP

 Hgrr3   KPWKMNLSKL   NMLKPDSDLC   LKFAMLCTLN   DKCDRLRKAY   GEACS.....
```

```
Rgrr3   KPWKMNLSKL SMLKPDSDLC LKFAMLCTLN DKCDRLRKAY GEACS.....


        201                                            250
Mgdnfr  NEVCNRRKCH KALRQFFDKV PAKHSYGMLF CSC..RDVAC TERRRQTIVP
Rgdnfr  NEVCNRRKCH KALRQFFDKV PAKHSYGMLF CSC..RDIAC TERRRQTIVP
Hgdnfr  NDVCNRRKCH KALRQFFDKV PAKHSYGMLF CSC..RDIAC TERRRQTIVP
 Hgrr2  TERCNRRKCH KALRQFFDRV PSEYTYRMLF CSC..QDQAC AERRRQTILP
 Rgrr2  TERCNRRKCH KALRQFFDRV PSEYTYRMLF CSC..QDQAC AERRRQTILP
 Hgrr3  GPHCQRHVCL RQLLTFFEKA AEPHAQGLLL CPCAPNDRGC GERRRNTIAP
 Rgrr3  GIRCQRHLCL AQLRSFFEKA AESHAQGLLL CPCAPEDAGC GERRRNTIAP
```

```
           251                                                      300
Mgdnfr     VCSYEERERP NCLNLQDSCK TNYICRSRLA DFFTNCQPES RSVSNCLKEN

Rgdnfr     VCSYEERERP NCLSLQDSCK TNYICRSRLA DFFTNCQPES RSVSNCLKEN

Hgdnfr     VCSYEEREKP NCLNLQDSCK TNYICRSRLA DFFTNCQPES RSVSSCLKEN

 Hgrr2     SCSYEDKEKP NCLDLRGVCR TDHLCRSRLA DFHANCRASY QTVTSCPADN

 Rgrr2     SCSYEDKEKP NCLDLRSLCR TDHLCRSRLA DFHANCRASY RTITSCPADN

 Hgrr3     NCALPP.VAP NCLELRRLCF SDPLCRSRLV DFQTHCHP.. MDILGTCATE

 Rgrr3     SCALPS.VAP NCLDLRSFCR ADPLCRSRLM DFQTHCHP.. MDILGTCATE


           301                                                      350
Mgdnfr     YADCLLAYSG LIGTVMTPNY VDSS..SLSV APWCDCSNSG NDLEDCLKFL

Rgdnfr     YADCLLAYSG LIGTVMTPNY VDSS..SLSV APWCDCSNSG NDLEDCLKFL

Hgdnfr     YADCLLAYSG LIGTVMTPNY IDSS..SLSV APWCDCSNSG NDLEECLKFL

 Hgrr2     YQACLGSYAG MIGFDMTPNY VDSSPTGIVV SPWCSCRGSG NMEEECEKFL

 Rgrr2     YQACLGSYAG MIGFDMTPNY VDSNPTGIVV SPWCNCRGSG NMEEECEKFL

 Hgrr3     QSRCLRAYLG LIGTAMTPNF ASNVNTSVAL S..CTCRGSG NLQEECEMLE

 Rgrr3     QSRCLRAYLG LIGTAMTPNF ISKVNTTVAL G..CTCRGSG NLQDECEQLE


           351                                                      400
Mgdnfr     NFFKDNTCLK NAIQAFGNGS DVTMWQPAP. PVQTTTATTT TAFRIKNKPS

Rgdnfr     NFFKDNTCLK NAIQAFGNGS DVTMWQPAP. PVQTTTATTT TAFRVKNKPL

Hgdnfr     NFFKDNTCLK NAIQAFGNGS DVTVWQPAF. PVQTTTATTT TALRVKNKPL

 Hgrr2     RDFTENPCLR NAIQAFGNGT NVNVSPKGP. SFQATQAPRV EKTPSLPDDL

 Rgrr2     RDFTENPCLR NAIQAFGNGT DVNMSPKGP. SLPATQAPRV EKTPSLPDDL

 Hgrr3     GFFSHNPCLT EAIAAKMRFH SQLFSQDWPH PTFAVMAHQN ENPAVRPQPW

 Rgrr3     KSFSQNPCLM EAIAAKMRFH RQLFSQDWAD STFSVMQQQN SSPALRPQLR


           401                                                      450
Mgdnfr     GPACSENEIP THVLPPCANL QAQKLKSNVS GSTHLCLSDN DYGKDGLAGA

Rgdnfr     GPAGSENEIP THVLPPCANL QAQKLKSNVS GSTHLCLSDS DFGKDGLAGA

Hgdnfr     GPAGSENEIP THVLPPCANL QAQKLKSNVS GNTHLCISNG NYEKEGL.GA

 Hgrr2     SDSTS...LG TSVITTCTSV QEQGLKANNS KELSMCFTEL TTNIIPGSNK

 Rgrr2     SDSTS...LG TSVITTCTSI QEQGLKANNS KELSMCFTEL TTNISPGSKK

 Hgrr3     VPSLFSCTLP LILLLSLW~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

 Rgrr3     LPVLSFFILT LILLQTLW*~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
```

```
        451                                    490
Mgdnfr  SSHITTKSMA APPSCGLSSL PVMVFTALAA LLSVSLAETS

Rgdnfr  SSHITTKSMA APPSCSLSSL PVLMLTALAA LLSVSLAETS

Hgdnfr  SSHITTKSMA APPSCGLSPL LVLVVTALST LLSLTETS~~

 Hgrr2  VIKPNSGPSR ARPSAALTVL SVLMLKLAL* ~~~~~~~~~~

 Rgrr2  VIKLNSGSSR ARLSAALTAL PLLMLTLAL* ~~~~~~~~~~

 Hgrr3  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

 Rgrr3  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
```

Figure 19
GDNFR Family of Receptors

```
          1                                                    50
Consensus MV..1...p .pp...m.1. 11slalPl.. .lqgael.g. .R1..dCv.A.
   Hgdnfr              MFLAT LYFALPLLDL LLSAEVSGGD RL..DCVKAS
   Rgdnfr              MFLAT LYFALPLLDL LMSAEVSGGD RL..DCVKAS
    Hgrr2      MILANVF CLFFFLDDTL RSLASPSS.. LQGPELHGW. RPPVDCVRAN
    Rgrr2          MLV FPSHYPDETL RSLASPSS.. LQGSELHGW. RPQVDCVRAN
    Hgrr3  MVRPLNPRPL PPVVLMLLLL LPPS.PLP.L AAGDPLPTES RLMNSCLQAR
    Rgrr3   MGLSRSPR PPPLVILLLV LSLWLPLG.. .TGNSLPTEN RLVNSCTQAR


          51                                                   100
Consensus ..C.ae..Cs ..YrtLrqC. ag...nt.La sg.E...... C..A.e.L..
   Hgdnfr DQCLKEQSCS TKYRTLRQCV AGKETNFSLA SGLEAKDE.. CRSAMEALKQ
   Rgdnfr DQCLKEQSCS TKYRTLRQCV AGKETNFSLT SGLEAKDE.. CRSAMEALKQ
    Hgrr2 ELCAAESNCS SRYRTLRQCL AGRDRNTMLA NK.E...... CQAALEVLQE
    Rgrr2 ELCAAESNCS SRYRTLRQCL AGRDRNTMLA NK.E...... CQAALEVLQE
    Hgrr3 RKCQADPTCS AAYHHLDSCT ..SSISTPLP SE.EPSVPAD CLEAAQQLRN
    Rgrr3 KKCEANPACK AAYQHLDSCT ..PSLSSPLP SG.ESATSAA CLEAAQQLRN


          101                                                  150
Consensus ssLydCrCkR gMKke..CL. IYWs.h..1. .Gn..le.SP YEp.VtSrls
   Hgdnfr KSLYNCRCKR GMKKEKNCLR IYWSMYQSLQ .GNDLLEDSP YEP.VNSRLS
   Rgdnfr KSLYNCRCKR GMKKEKNCLR IYWSMYQSLQ .GNDLLEDSP YEP.VNSRLS
    Hgrr2 SPLYDCRCKR GMKKELQCLQ IYWSIHLGLT EGEEFYEASP YEP.VTSRLS
    Rgrr2 SPLYDCRCKR GMKKELQCLQ IYWSIHLGLT EGEEFYEASP YEP.VTSRLS
    Hgrr3 SSLIGCMCHR RMKNQVACLD IYWTVHRARS LGNYELDVSP YEDTVTSKPW
    Rgrr3 SSLIDCRCHR RMKHQATCLD IYWTVHPVRS LGDYELDVSP YEDTVTSKPW
```

```
            151                                                          200
Consensus   difr..s..s  ....d.....  ksn.CLdaAk  aCnLnD.Ckk  lRsaYi..C.
  Hgdnfr    DIFRVVPFIS  DVFQQVEHIP  KGNNCLDAAK  ACNLDDICKK  YRSAYITPCT
  Rgdnfr    DIFRAVPFIS  DVFQQVEHIS  KGNNCLDAAK  ACNLDDTCKK  YRSAYITPCT
  Hgrr2     DIFRLASIFS  GTGADPVVSA  KSNHCLDAAK  ACNLNDNCKK  LRSSYISICN
  Rgrr2     DIFRLASIFS  GTGTDPAVST  KSNHCLDAAK  ACNLNDNCKK  LRSSYISICN
  Hgrr3     KMNL..SKLN  MLKPD.....  .SDLCLKFAM  LCTLNDKCDR  LRKAYGEAC.
  Rgrr3     KMNL..SKLS  MLKPD.....  .SDLCLKFAM  LCTLNDKCDR  LRKAYGEAC.


            201                                                          250
Consensus   ...S..erCn  RrkChkaLrq  FFdkvp..h.  ygmLfCsC..  .D.aC.ERRR
  Hgdnfr    TSVS.NDVCN  RRKCHKALRQ  FFDKVPAKHS  YGMLFCSC..  RDIACTERRR
  Rgdnfr    TSMS.NEVCN  RRKCHKALRQ  FFDKVPAKHS  YGMLFCSC..  RDIACTERRR
  Hgrr2     REISPTERCN  RRKCHKALRQ  FFDRVPSEYT  YRMLFCSC..  QDQACAERRR
  Rgrr2     REISPTERCN  RRKCHKALRQ  FFDRVPSEYT  YRMLFCSC..  QDQACAERRR
  Hgrr3     ...SG.PHCQ  RHVCLRQLLT  FFEKAAEPHA  QGLLLCPCAP  NDRGCGERRR
  Rgrr3     ...SG.IRCQ  RHLCLAQLRS  FFEKAAESHA  QGLLLCPCAP  EDAGCGERRR


            251                                                          300
Consensus   qTI.PsCsye  ..ekPNCLdL  r..Crtd.lC  RSRLaDF.tn  C....r.v.s
  Hgdnfr    QTIVPVCSYE  EREKPNCLNL  QDSCKTNYIC  RSRLADFFTN  CQPESRSVSS
  Rgdnfr    QTIVPVCSYE  ERERPNCLSL  QDSCKTNYIC  RSRLADFFTN  CQPESRSVSN
  Hgrr2     QTILPSCSYE  DKEKPNCLDL  RGVCRTDHLC  RSRLADFHAN  CRASYQTVTS
  Rgrr2     QTILPSCSYE  DKEKPNCLDL  RSLCRTDHLC  RSRLADFHAN  CRASYRTITS
  Hgrr3     NTIAPNC.AL  PPVAPNCLEL  RRLCFSDPLC  RSRLVDFQTH  C.HPMDILGT
  Rgrr3     NTIAPSC.AL  PSVAPNCLDL  RSFCRADPLC  RSRLMDFQTH  C.HPMDILGT


            301                                                          350
Consensus   C.a.ny..CL  .aY.GlIGt.  MTPNyvdss.  t...VapwC.  CrgSGN..ee
  Hgdnfr    CLKENYADCL  LAYSGLIGTV  MTPNYIDSSS  ..LSVAPWCD  CSNSGNDLEE
  Rgdnfr    CLKENYADCL  LAYSGLIGTV  MTPNYVDSSS  ..LSVAPWCD  CSNSGNDLED
  Hgrr2     CPADNYQACL  GSYAGMIGFD  MTPNYVDSSP  TGIVVSPWCS  CRGSGNMEEE
  Rgrr2     CPADNYQACL  GSYAGMIGFD  MTPNYVDSNP  TGIVVSPWCN  CRGSGNMEEE
  Hgrr3     C.ATEQSRCL  RAYLGLIGTA  MTPNFASNVN  TS..VALSCT  CRGSGNLQEE
  Rgrr3     C.ATEQSRCL  RAYLGLIGTA  MTPNFISKVN  TT..VALGCT  CRGSGNLQDE
```

```
                351                                                          400
Consensus       Cekfl.fF..  NpCL.nAIqA  fgng......  .....p.fsv  .....t.t.a
   Hgdnfr       CLKFLNFFKD  NTCLKNAIQA  FGNGS....D  VTVWQPAFPV  QTTTATTTTA
   Rgdnfr       CLKFLNFFKD  NTCLKNAIQA  FGNGS....D  VTMWQPAPPV  QTTTATTTTA
    Hgrr2       CEKFLRDFTE  NPCLRNAIQA  FGNGTNV...  ......NVSP  KGPSFQATQA
    Rgrr2       CEKFLRDFTE  NPCLRNAIQA  FGNGTDV...  ......NMSP  KGPSLPATQA
    Hgrr3       CEMLEGFFSH  NPCLTEAIAA  KMRFHSQLFS  QDWPHPTFAV  MAHQNENPAV
    Rgrr3       CEQLEKSFSQ  NPCLMEAIAA  KMRFHRQLFS  QDWADSTFSV  MQQQNSSPAL


                401                                                          450
Consensus       .rv...PsL.  ...s....l.  t.v...C..l  Q.Q.LK.N.S  .e...Cf.el
   Hgdnfr       LRVKNKP.LG  PAGSENEIP.  THVLPPCANL  QAQKLKSNVS  GNTHLCISNG
   Rgdnfr       FRVKNKP.LG  PAGSENEIP.  THVLPPCANL  QAQKLKSNVS  GSTHLCLSDS
    Hgrr2       PRVEKTPSLP  DDLSDSTSLG  TSVITTCTSV  QEQGLKANNS  KELSMCFTEL
    Rgrr2       PRVEKTPSLP  DDLSDSTSLG  TSVITTCTSI  QEQGLKANNS  KELSMCFTEL
    Hgrr3       RPQPWVPSLF  SCTLPLILLL  SLW
    Rgrr3       RPQLRLPVLS  FFILTLILLQ  TLW


                451                                                     499
Consensus       ttn....sg.  ...i...s..  A.pS.aL..L  pvlmltala.  LLS....S
   Hgdnfr       NYEKEGL.GA  SSHITTKSMA  APPSCGLSPL  LVRVVTALST  LLSLTETS
   Rgdnfr       DFGKDGLAGA  SSHITTKSMA  APPSCSLSSL  PVLMLTALAA  LLSVSLA
    Hgrr2       TTNIIPGSNK  VIKPNSGPSR  ARPSAALTVL  SVLMLK.LAL
    Rgrr2       TTNISPGSKK  VIKLNSGSSR  ARLSAALTAL  PLLMLTLAL
```

Figure 20

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Human GDNFRα              MFLATLYFALPLLDLLLSAEVSGGDRLDCVKASDQCLKE
Rat GDNFRα                MFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKE
Human GRR2      MILANVFCLFFFLDDTLRSLASPSSLQGPELHGWRPPVDCVRANELCAAE
Rat GRR2        MLVFPSHYPDETLRSLASPSSLQGSELHGWRPQVDCVRANELCAAE

Human GDNFRα    QSCSTKYRTLRQCVAGKETNFSLASGLEAKDECRSAMEALKQKSLYNCRC
Rat GDNFRα      QSCSTKYRTLRQCVAGKETNFSLTSGLEAKDECRSAMEALKQKSLYNCRC
Human GRR2      SNCSSRYRTLRQCLAGRDRN.....TMLANKECQAALEVLQESPLYDCRC
Rat GRR2        SNCSSRYRTLRQCLAGRDRN.....TMLANKECQAALEVLQESPLYDCRC

Human GDNFRα    KRGMKKEKNCLRIYWSMYQSL.QGNDLLEDSPYEPVNSRLSDIFRVVPFI
Rat GDNFRα      KRGMKKEKNCLRIYWSMYQSL.QGNDLLEDSPYEPVNSRLSDIFRAVPFI
Human GRR2      KRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRLASIF
Rat GRR2        KRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRLASIF

Human GDNFRα    SDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAYITPCTTSVS.NDVC
Rat GDNFRα      SDVFQQVEHISKGNNCLDAAKACNLDDTCKKYRSAYITPCTTSMS.NEVC
Human GRR2      SGTGADPVVSAKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERC
Rat GRR2        SGTGTDPAVSTKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERC

Human GDNFRα    NRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRQTIVPVCSYEE
Rat GDNFRα      NRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRQTIVPVCSYEE
Human GRR2      NRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYED
Rat GRR2        NRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYED

Human GDNFRα    REKPNCLNLQDSCKTNYICRSRLADFFTNCQPESRSVSSCLKENYADCLL
Rat GDNFRα      RERPNCLSLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLL
Human GRR2      KEKPNCLDLRGVCRTDHLCRSRLADFHANCRASYQTVTSCPADNYQACLG
Rat GRR2        KEKPNCLDLRSLCRTDHLCRSRLADFHANCRASYRDITSCPADNYQACLG

Human GDNFRα    AYSGLIGTVMTPNYIDSS...SLSVAPWCDCSNSGNDLEECLKFLNFFKDN
Rat GDNFRα      AYSGLIGTVMTPNYVDSS...SLSVAPWCDCSNSGNDLEDCLKFLNFFKDN
Human GRR2      SYAGMIGFDMTPNYVDSSPTGIVVSPWCSCRGSGNMEEECEKFLRDFTEN
Rat GRR2        SYAGMIGFDMTPNYVDSNPTGIVVSPWCNCRGSGNMEEECEKFLRDFTEN

Human GDNFRα    TCLKNAIQAFGNGSDVTVWQPAFPVQTTTATTTTALRVKNKPLGPAGSEN
Rat GDNFRα      TCLKNAIQAFGNGSDVTMWQPAPPVQTTTATTTTAFRVKNKPLGPAGSEN
Human GRR2      PCLRNAIQAFGNGTNVNVSPKGPSFQATQAPRVEKTPSLPDDLSDSTS..
Rat GRR2        PCLRNAIQAFGNGTDVNMSPKGPSLPATQAPRVEKTPSLPDDLSDSTS..

Human GDNFRα    EIPTHVLPPCANLQAQKLKSNVSGNTHLCISNGNYEKEGL.GASSHITTK
Rat GDNFRα      EIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDSDFGKDGLAGASSHITTK
Human GRR2      .LGTSVITTCTSVQEQGLKANNSKELSMCFTELTTNIIPGSNKVIKPNSG
Rat GRR2        .LGTSVITTCTSIQEQGLKANNSKELSMCFTELTTNISPGSKKVIKLNSG

Human GDNFRα    SMAAPPSCGLSPLLVLVVT.ALSTLL..SLIETS
Rat GDNFRα      SMAAPPSCSLSSLPVLMLT.ALAALLSVSLAETS
Human GRR2      PSRARPSAALTVLSVLMLKLAL
Rat GRR2        SSRARLSAALTALPLLMLTLAL
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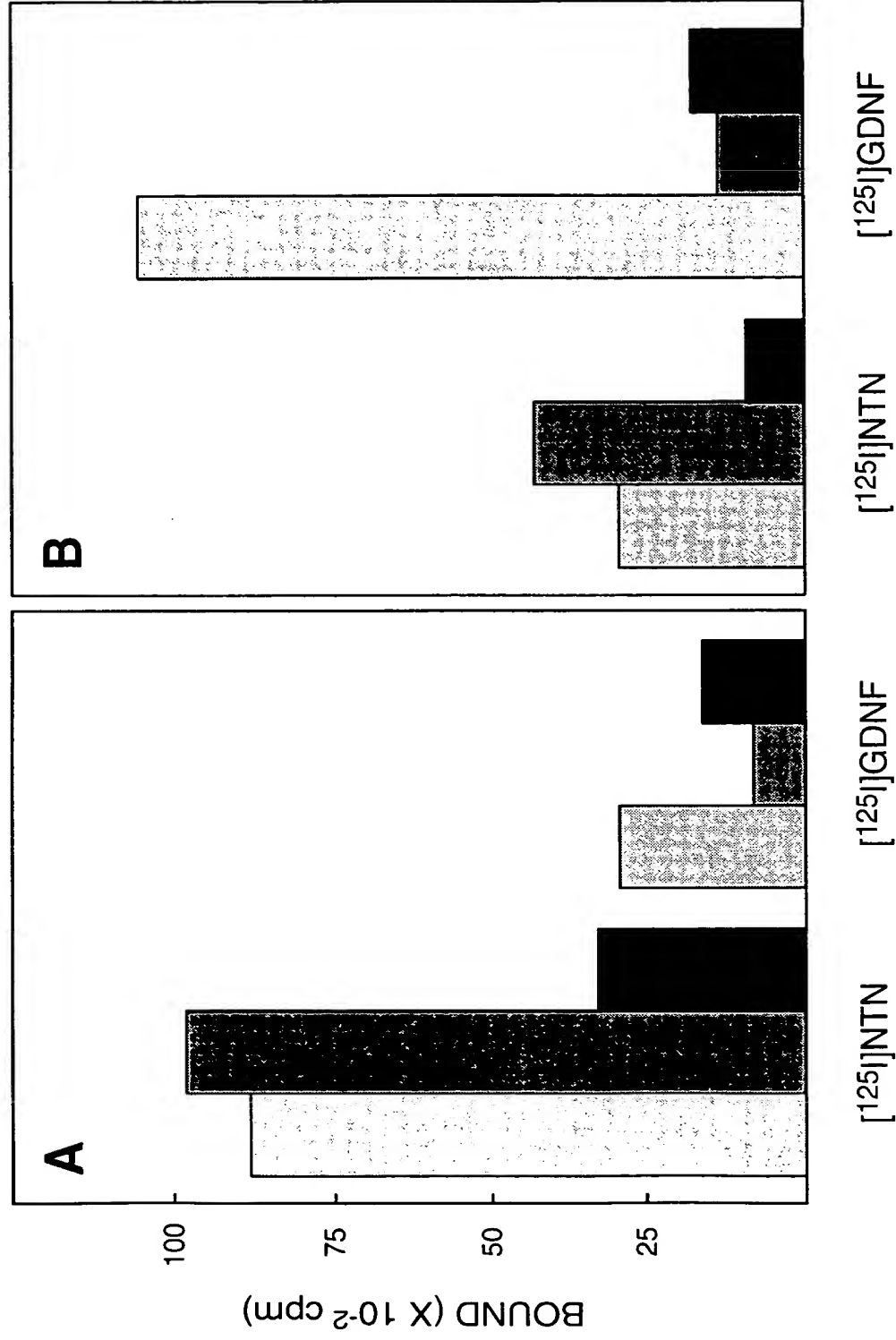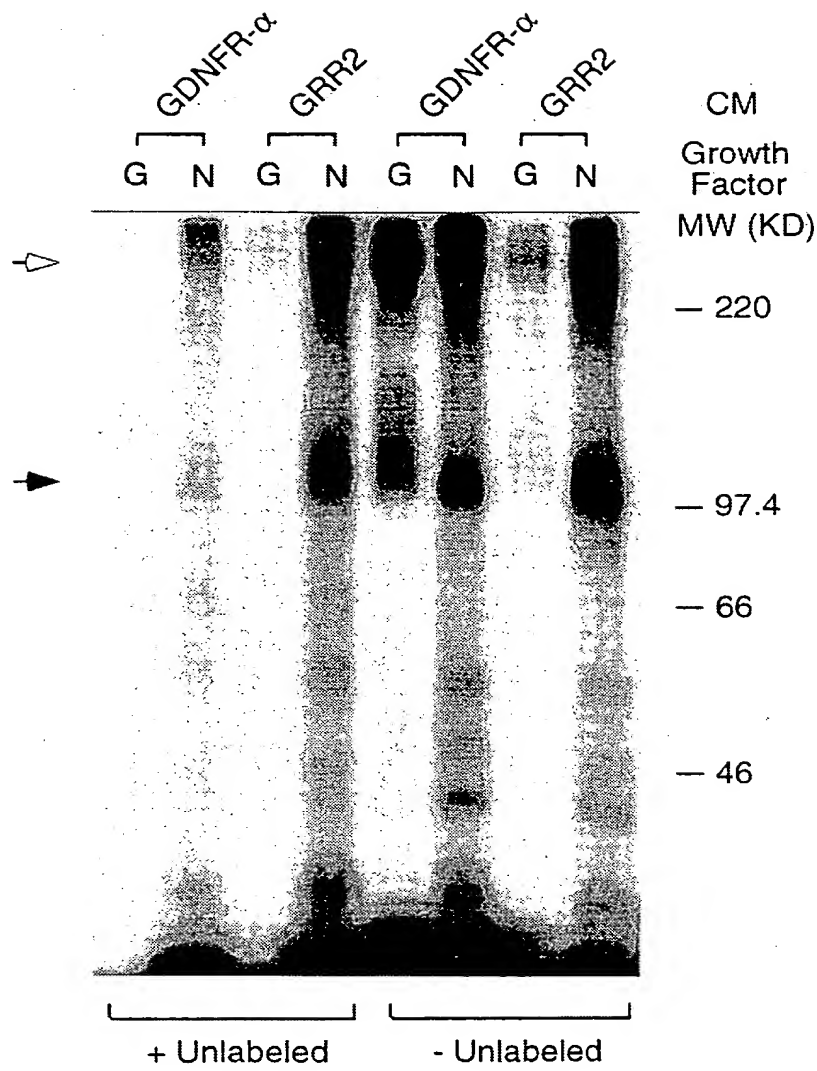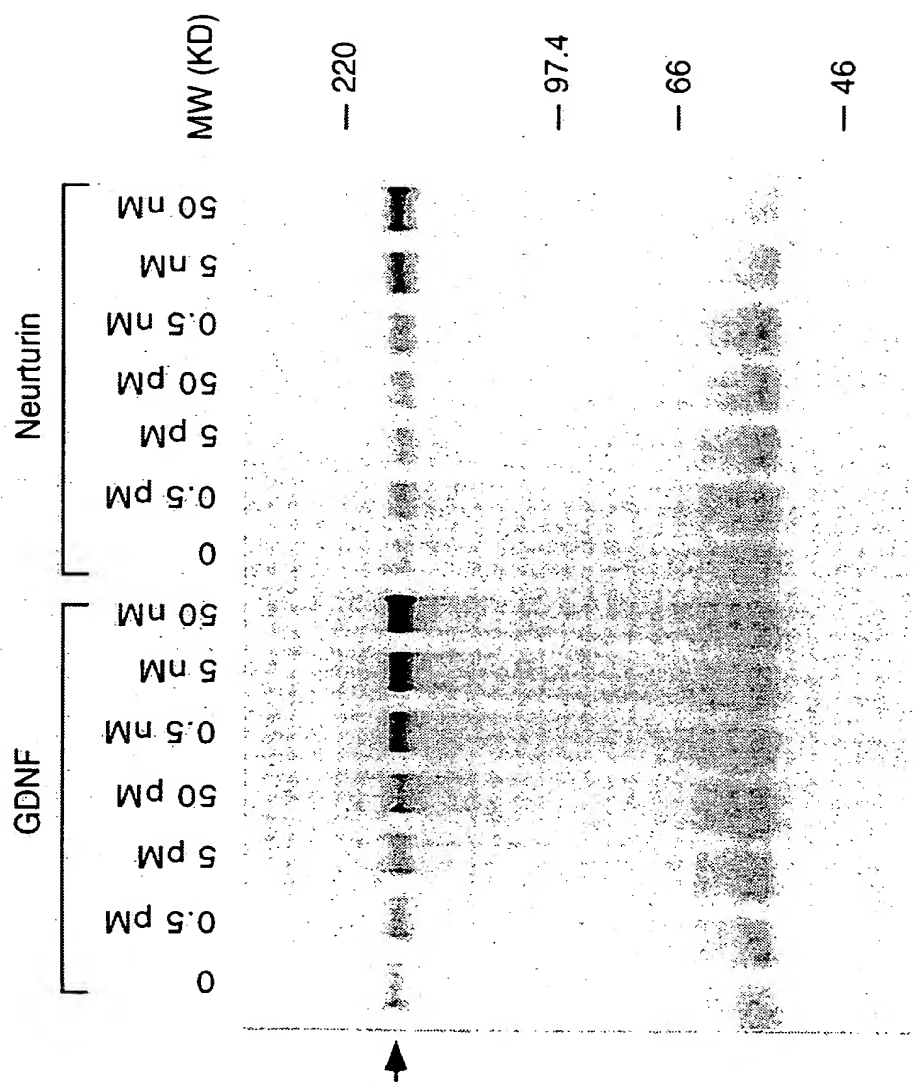
Figure 21

Figure 22

CM
Growth
Factor
MW (KD)

— 220

— 97.4

— 66

— 46

+ Unlabeled   - Unlabeled

Figure 23

Figure 24

MW
(KD)

— 220

— 97.4

— 66

— 46

Neurturin

50 nM
5 nM
0.5 nM
50 pM
5 pM
0.5 pM
0

GDNF

50 nM
5 nM
0.5 nM
50 pM
5 pM
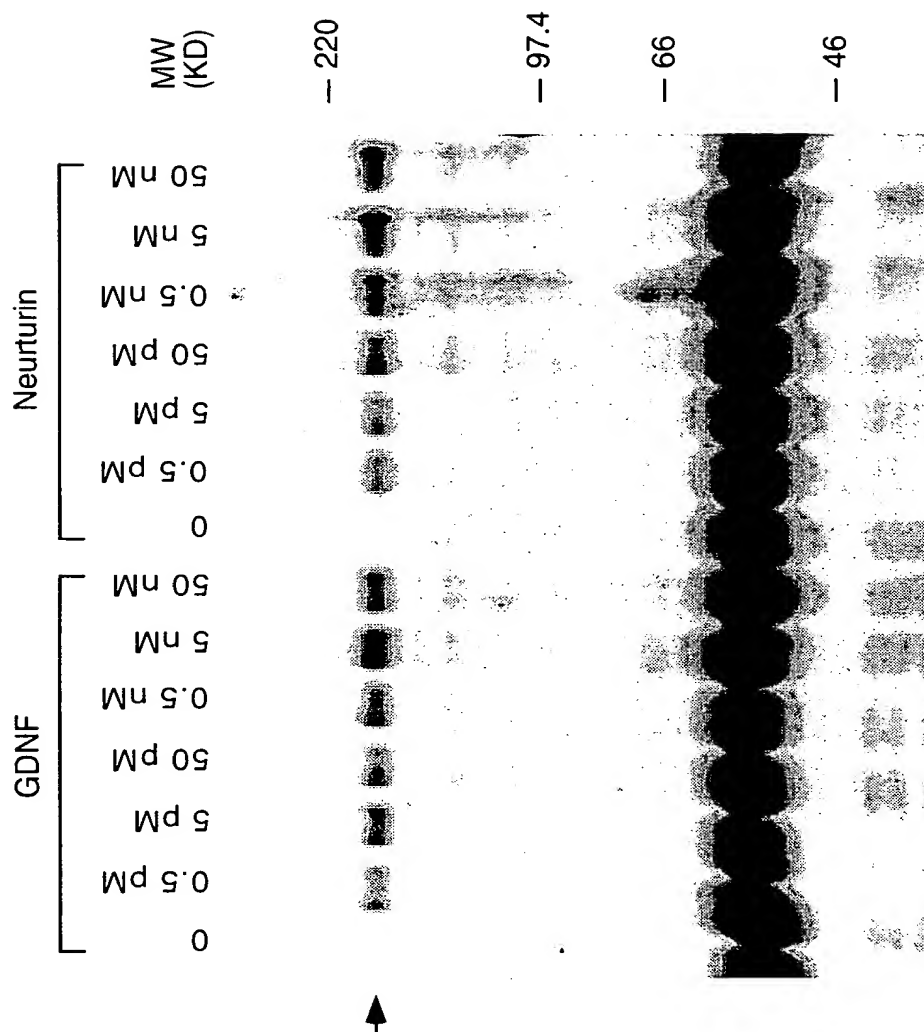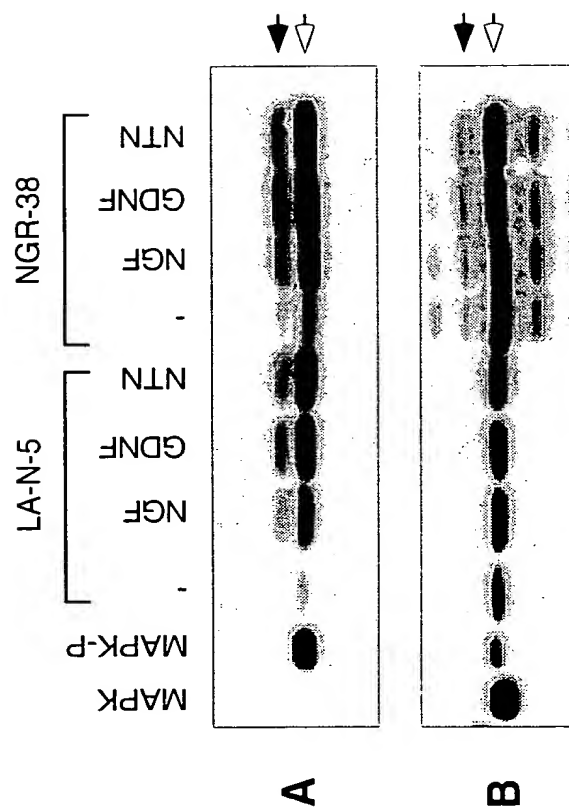0.5 pM
0

Figure 25

Figure 26

```
          1                                                          50
CONSENSUS .........P ....l.tl.s l..pl.l..S .....r...d Cv.A...C.a
    GDNFR .......... ..MFLATLYF ALPLLDLLMS AEVSGGDRLD CVKASDQCLK
     GRR2 .....MLVFP SHYPDETLRS LASPSSLQGS ELHGWRPQVD CVRANELCAA
     GRR3 MGLSRSPRPP PLVILLLVLS LWLPLGTGNS LPTENRLVNS CTQARKKCEA

          51         Cs..Yrt                                        100
CONSENSUS e..Cs..Yrt LrqC.ag... n........a ..eC..A.e. L..ssLydCR
    GDNFR EQSCSTKYRT LRQCVAGKET NFSLTSGLEA KDECRSAMEA LKQKSLYNCR
     GRR2 ESNCSSRYRT LRQCLAGRDR N.....TMLA NKECQAALEV LQESPLYDCR
     GRR3 NPACKAAYQH LDSCTPSLSS PLPSGES.AT SAACLEAAQQ LRNSSLIDCR

          101                                                        150
CONSENSUS CkRgMKke.. CL.IYWs.h. .l..G...le .SPYE.pVtS rlsdifr..s
    GDNFR CKRGMKKEKN CLRIYWSMYQ SL.QGNDLLE DSPYE.PVNS RLSDIFRAVP
     GRR2 CKRGMKKELQ CLQIYWSIHL GLTEGEEFYE ASPYE.PVTS RLSDIFRLAS
     GRR3 CHRRMKHQAT CLDIYWTVHP VRSLGDYELD VSPYEDTVTS ..KPWKMNLS

          151                                                        200
CONSENSUS ..S....d.. ...ksn.CLd aAkaCnLnD. Ckkl RsaYi. .C....S...e
    GDNFR FISDVFQQVE HISKGNNCLD AAKACNLDDT CKKYRSAYIT PCTTSMS.NE
     GRR2 IFSGTGTDPA VSTKSNHCLD AAKACNLNDN CKKLRSSYIS ICNREISPTE
     GRR3 KLSMLKPD.. ....SDLCLK FAMLCTLNDK CDRLRKAYGE AC....SG.I

          201                                                        250
CONSENSUS rCnRrkChka LRqFFdkvp. .h.ygmLfCs C...D.aC.E RRRqTI.PsC
    GDNFR VCNRRKCHKA LRQFFDKVPA KHSYGMLFCS C..RDIACTE RRRQTIVPVC
     GRR2 RCNRRKCHKA LRQFFDRVPS EYTYRMLFCS C..QDQACAE RRRQTILPSC
     GRR3 RCQRHLCLAQ LRSFFEKAAE SHAQGLLLCP CAPEDAGCGE RRRNTIAPSC

          251                                                        300
CONSENSUS sye..e.PNC LdLrs.Crtd .lCRSRLaDF .tnC.p..r. .t.C.a.ny.
    GDNFR SYEERERPNC LSLQDSCKTN YICRSRLADF FTNCQPESRS VSNCLKENYA
     GRR2 SYEDKEKPNC LDLRSLCRTD HLCRSRLADF HANCRASYRT ITSCPADNYQ
     GRR3 ALPSVA.PNC LDLRSFCRAD PLCRSRLMDF QTHCHPMDIL GT.C.ATEQS

          301                                                        350
CONSENSUS .CL.aY.GlI Gt.MTPNyvd s..t...Vap wC.CrgSGN. .eeCekfl..
    GDNFR DCLLAYSGLI GTVMTPNYVD SSSL..SVAP WCDCSNSGND LEDCLKFLNF
     GRR2 ACLGSYAGMI GFDMTPNYVD SNPTGIVVSP WCNCRGSGNM EEECEKFLRD
     GRR3 RCLRAYLGLI GTAMTPNFIS KVNTT..VAL GCTCRGSGNL QDECEQLEKS

          351                                                        400
CONSENSUS F..NpCL.nA IqAfgng.dv .msq..p... .t.a..... rv...p.l..
    GDNFR FKDNTCLKNA IQAFGNGSDV TMWQPAPPVQ TTTATTTTAF RVKNKP.LGP
     GRR2 FTENPCLRNA IQAFGNGTDV NMSPKGPSLP ATQAP..... RVEKTPSLPD
     GRR3 FSQNPCLMEA IAAKMRFHRQ LFSQDWADST FSVMQQQNSS PALRPQ....

          401                                                        450
CONSENSUS ..s......t .v...c...q .q.lk.n.s. ....c..... ..........
    GDNFR AGS.ENEIPT HVLPPCANLQ AQKLKSNVSG STHLCLSDSD FGKDGLAGAS
     GRR2 DLSDSTSLGT SVITTCTSIQ EQGLKANNSK ELSMCFTELT TNISPGSKKV
     GRR3 .......... .......... .......... .......... ..........

          451                          489
CONSENSUS ......s..a ..s..l..LP vLmlt.l... l...l.ets
    GDNFR SHITTKSMAA PPSCSLSSLP VLMLTALAAL LSVSLAETS
     GRR2 IKLNSGSSRA RLSAALTALP LLMLTLAL
     GRR3 .......... .....LRLP VLSFFILTLI LLQTLW
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